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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:06:35 ; Search time 15 Seconds
(without alignments)
82.384 Million cell updates/sec

Title: US-09-580-018-42
Perfect score: 217
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSKGAIIGLMVGGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing-first-45-summaries

Database: Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	217	100.0	42	1	US-07-744-767A-2
2	217	100.0	42	1	US-08-179-574-1
3	217	100.0	42	1	US-08-347-144-1
4	217	100.0	42	1	US-08-462-859A-19
5	217	100.0	42	1	US-08-123-659A-19
6	217	100.0	42	1	US-08-464-247A-19
7	217	100.0	42	1	US-08-464-248A-19
8	217	100.0	42	1	US-08-476-464A-1
9	217	100.0	42	1	US-08-304-585-2
10	217	100.0	42	1	US-08-302-808-5
11	217	100.0	42	1	US-08-268-348A-1
12	217	100.0	42	1	US-08-433-734-2
13	217	100.0	42	2	US-08-609-090-9
14	217	100.0	42	2	US-07-737-371E-72
15	217	100.0	42	2	US-08-422-333-4
16	217	100.0	42	2	US-08-682-245A-4
17	217	100.0	42	2	US-08-986-948-5
18	217	100.0	42	3	US-08-717-551A-2
19	217	100.0	42	4	US-09-388-890-1
20	217	100.0	42	4	US-09-005-215-20
21	217	100.0	42	4	US-09-242-724-23
22	217	100.0	42	4	US-08-922-930-2
23	217	100.0	42	5	PCT-US92-06700-2
24	217	100.0	42	5	PCT-US93-00325-1
25	217	100.0	43	1	US-08-235-400-1
26	217	100.0	43	1	US-08-437-067-1
27	217	100.0	43	1	US-08-302-808-6

28	217	100.0	43	1	US-08-079-511-1	Sequence 1, Appli
29	217	100.0	43	1	US-08-467-607-1	Sequence 1, Appli
30	217	100.0	43	2	US-08-404-831-1	Sequence 1, Appli
31	217	100.0	43	2	US-08-602-264A-3	Sequence 3, Appli
32	217	100.0	43	2	US-08-469-362-1	Sequence 1, Appli
33	217	100.0	43	2	US-08-612-785B-1	Sequence 1, Appli
34	217	100.0	43	2	US-08-475-579A-1	Sequence 1, Appli
35	217	100.0	43	2	US-08-850-392-1	Sequence 1, Appli
36	217	100.0	43	2	US-07-737-371E-70	Sequence 70, Appli
37	217	100.0	43	2	US-08-986-948-6	Sequence 6, Appli
38	217	100.0	43	2	US-08-975-977-1	Sequence 1, Appli
39	217	100.0	43	2	US-08-817-423-1	Sequence 1, Appli
40	217	100.0	43	2	US-08-920-162A-1	Sequence 1, Appli
41	217	100.0	43	3	US-08-461-018A-3	Sequence 3, Appli
42	217	100.0	43	3	US-08-976-191-1	Sequence 1, Appli
43	217	100.0	43	3	US-08-976-179-1	Sequence 1, Appli
44	217	100.0	43	4	US-09-216-958-3	Sequence 3, Appli
45	217	100.0	43	4	US-09-356-931-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-744-767A-2
; Sequence 2, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Reptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.236-US-01
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-744-767A-2

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIA 42

RESULT 2

US-08-179-574-1
; Sequence 1, Application US/08179574
; Patent No. 5506097
; GENERAL INFORMATION:
; APPLICANT: Huntington Potter
; APPLICANT: Usamah Kayyali
; TITLE OF INVENTION: Compounds and Methods for Inhibiting
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/819,361
; FILING DATE: 13-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU90-03A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-179-574-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIA 42
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DB 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIA 42

RESULT 3

US-08-347-144-1
; Sequence 1, Application US/08347144
; Patent No. 5589154
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,144

FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIA 42
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DB 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIA 42

RESULT 4

US-08-462-859A-19
; Sequence 19, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-19

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: STREET: One Campus Drive
: CITY: Parsippany
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07054
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-683-2158
: TELEFAX: 201-683-4117
:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
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: US-08-464-247A-19
:
: Query Match 100.0%; Score 217; DB 1;
: Best Local Similarity 100.0%; Pred. No. 4e-26;
: Matches 42; Conservative 0; Mismatches 0;
:
: QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIA 4
: Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIA 4
:
: RESULT 7
: US-08-464-248A-19
: Sequence-19, Application US/08464248A
: Patent No. 5703209
: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: APPLICANT: Vitek, M. P.
: TITLE OF INVENTION: No. 5703209el Amyloid Precursors
: TITLE OF INVENTION: Using Same to Access Agents V
: TITLE OF INVENTION: of B-Amyloid Peptide
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSER: American Cyanamid Company
: STREET: One Cyanamid Plaza
: CITY: Wayne
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07470-8426
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)831-3246
: TELEFAX: (201)831-3305

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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106

GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 10
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: OAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 13-SEP-1994

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICANT: Dobe, Heinz
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 010132/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 28-DEC-1993
APPLICATION NUMBER: 334773/1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
STREET: 200291 STRE
CITY: New Jersey
STATE: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11
US-08-268-348A-1
Sequence 1, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobe, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 12
US-08-433-734-2
Sequence 2, Application US/08433734
Patent No. 5837473
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyn, Patrick W.
TITLE OF INVENTION: Labelled
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-2

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

RESULT 13

US-08-609-090-9

; Sequence 9, Application US/08609090

; Patent No. 5840838

; GENERAL INFORMATION:

; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.

; APPLICANT: CARNEY, John M.

; APPLICANT: AKSENOV, Michael

; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LOWE PRICE LEBLANC & BECKER

; STREET: 99 Canal Center Plaza, Suite 300

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/609,090

; FILING DATE: 29-FEB-1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kraus, Eric J.

; REGISTRATION NUMBER: 36,190

; REFERENCE/DOCKET NUMBER: 434-059

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-684-1111

; TELEFAX: 703-684-1124

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-609-090-9

Query Match 100.0%; Score 217; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 4e-26;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
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RESULT 14

US-07-737-371E-72

; Sequence 72, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-737-371E-72

Query Match 100.0%; Score 217; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 4e-26;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

RESULT 15

US-08-422-333-4

; Sequence 4, Application US/08422333

; Patent No. 5912410

; GENERAL INFORMATION:

; APPLICANT: CORDELL, Barbara L.

; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING

; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scios, Inc.

; STREET: 2450 Bayshore Parkway

; CITY: Mountain View

; STATE: CA

; COUNTRY: USA

; ZIP: 94043

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,333

; FILING DATE: 13-APR-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Shearer, Peter R.

; REGISTRATION NUMBER: 28,117

; REFERENCE/DOCKET NUMBER: 21900-28048.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 966-1550

; TELEFAX: (415) 968-2438

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 amino acids

; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Search completed: April 21, 2003, 12:08:07
Job time : 16 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run On: April 21, 2003, 12:06:50 ; Search time 15 Seconds
(without alignments)
211.719 Million cell updates/sec

Title: US-09-580-018-42

Perfect-score: 217

Sequence: 1 DAEPHDSGVVHHQKLVFF.....DVGSNKGAILGLMVGWVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	100.0	42	8	US-08-923-055-2
2	217	100.0	42	9	US-10-051-496-2
3	217	100.0	42	9	US-10-082-804-7
4	217	100.0	42	9	US-09-962-950C-37
5	217	100.0	42	9	US-09-848-616-174
6	217	100.0	42	9	US-09-865-294-65
7	217	100.0	42	10	US-09-867-847-1
8	217	100.0	42	10	US-09-956-625-26
9	217	100.0	42	10	US-09-731-460-1
10	217	100.0	43	9	US-10-076-708-7
11	217	100.0	43	9	US-10-051-496-1
12	217	100.0	43	9	US-10-217-459-1
13	217	100.0	43	10	US-09-280-966-1
14	217	100.0	43	10	US-09-904-987-1
15	217	100.0	43	10	US-09-808-037-3
16	217	100.0	43	10	US-09-866-712-3
17	217	100.0	43	10	US-09-972-475-1
18	217	100.0	43	10	US-09-992-800-1
19	217	100.0	43	10	US-09-895-443-1

20	217	100.0	43	10	US-09-996-357-1	Sequence 1, Appli
21	217	100.0	43	10	US-09-992-994-1	Sequence 1, Appli
22	217	100.0	43	10	US-09-984-834-1	Sequence 1, Appli
23	217	100.0	43	12	US-10-041-605-1	Sequence 1, Appli
24	217	100.0	53	10	US-09-797-543-5	Sequence 5, Appli
25	217	100.0	53	12	US-10-016-717-1	Sequence 1, Appli
26	217	100.0	70	10	US-09-153-076-14	Sequence 14, Appli
27	217	100.0	82	9	US-09-848-616-173	Sequence 173, App
28	217	100.0	99	9	US-10-183-119-2	Sequence 2, Appli
29	217	100.0	100	10	US-09-794-975-4	Sequence 4, Appli
30	217	100.0	103	10	US-09-972-475-2	Sequence 2, Appli
31	217	100.0	103	10	US-09-895-443-2	Sequence 2, Appli
32	217	100.0	117	9	US-09-422-569-10	Sequence 10, Appli
33	217	100.0	117	10	US-09-794-975-6	Sequence 6, Appli
34	217	100.0	117	10	US-09-823-153-2	Sequence 2, Appli
35	217	100.0	355	10	US-09-794-975-13	Sequence 13, Appli
36	217	100.0	695	10	US-09-794-927-10	Sequence 10, Appli
37	217	100.0	695	10	US-09-794-927-12	Sequence 12, Appli
38	217	100.0	695	10	US-09-794-927-14	Sequence 14, Appli
39	217	100.0	695	10	US-09-795-847-10	Sequence 10, Appli
40	217	100.0	695	10	US-09-795-847-12	Sequence 12, Appli
41	217	100.0	695	10	US-09-795-847-14	Sequence 14, Appli
42	217	100.0	695	10	US-09-794-743-10	Sequence 10, Appli
43	217	100.0	695	10	US-09-794-743-12	Sequence 12, Appli
44	217	100.0	695	10	US-09-794-743-14	Sequence 14, Appli
45	217	100.0	695	10	US-09-794-748-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-923-055-2
; Sequence 2, Application US/08923055
; Patent No. US20010016327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Glilian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: & No. US20010016327A1RIS LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,055
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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US-08-923-055-2
Query Match      100.0%; Score 217; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 2
US-10-051-496-2
; Sequence 2, Application US/10051496
; Publication No. US20020182660A1
; GENERAL INFORMATION:
; APPLICANT: Kel-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
; Abeta(1-41), Abeta(1-42) and Abeta(1-43)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kel-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 Inch, 1.44MB storage
; COMPUTER: IBM PC Compatibles
; OPERATING SYSTEM: Windows
; SOFTWARE: MS No. US20020182660A1epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051,496
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,854A
; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 60/183,407
; FILING DATE: 18-February-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Koenig, C. Frederick III
; REGISTRATION NUMBER: 29,662
; REFERENCE/DOCKET NUMBER: PBI-PT001.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-6400
; TELEFAX: (215) 568-6499
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 Amino Acid
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1-42
; IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2:FROM 1-42
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-051-496-2
Query Match      100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 3
US-10-082-804-7
; Sequence 7, Application US/10082804
; Publication No. US20020194632A1
; GENERAL INFORMATION:
; APPLICANT: McConlogue, Lisa
; APPLICANT: Gurney, Mark E.
; TITLE OF INVENTION: Transgenic Knockouts of BACE-1
; FILE REFERENCE: MBHB 02-329-A
; CURRENT APPLICATION NUMBER: US/10/082,804
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/271,092
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/271,514
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/293,762
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7
Query Match      100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 4
US-09-962-955C-37
; Sequence 37, Application US/09962955C
; Publication No. US20030013648A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo M. Castillo
; APPLICANT: Alan D. Snow
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: ProteoTech, Inc, 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 Inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: Windows 98
; SOFTWARE: WordPerfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,955C
; FILING DATE: 24-September-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/938,275
; FILING DATE: 22-August-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROEO.P03CI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: Also referred to in the specification as "AB 1-42"
US-09-962-955C-37

Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 5
US-09-848-616-174
; Sequence 174, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
US-09-848-616-174

Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 6
US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 65
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-65

Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 7
US-09-867-847-1
; Sequence 1, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-1

Query Match 100.0%; Score 217; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-09-956-625-26
; Sequence 26, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-625-26
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Search completed: April 21, 2003, 12:08:28
Job time : 15 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:48 ; Search time 11.5 Seconds
(without alignments)
25.585 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFHRDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68033

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	10	1	US-08-371-930-12
2	9	90.0	10	5	PCT-US94-01712-12
3	5	50.0	5	4	US-08-617-267C-36
4	4	40.0	6	1	US-07-843-949A-8
5	4	40.0	6	2	US-08-218-978-8
6	4	40.0	7	3	US-08-303-861-3
7	4	40.0	7	4	US-09-173-941-82
8	4	40.0	9	6	5177197-3
9	4	40.0	10	1	US-07-766-351-1
10	4	40.0	10	1	US-08-059-032-1
11	4	40.0	10	2	US-08-764-640-119
12	4	40.0	10	2	US-08-659-984A-19
13	4	40.0	10	3	US-08-973-225-119
14	4	40.0	10	3	US-09-244-298A-119
15	4	40.0	10	4	US-08-480-332-9
16	4	40.0	10	4	US-08-660-531-19
17	4	40.0	10	4	US-09-516-704-119
18	4	40.0	10	4	US-09-548-372D-63
19	4	40.0	10	4	US-09-548-372D-64
20	4	40.0	10	4	US-09-548-367D-63
21	4	40.0	10	4	US-09-548-367D-64
22	4	40.0	10	4	US-09-549-090-119
23	4	40.0	10	5	PCT-US91-07290-1
24	3	30.0	5	1	US-07-750-330-1
25	3	30.0	5	1	US-07-750-330-2
26	3	30.0	5	1	US-07-750-330-5
27	3	30.0	5	1	US-07-780-790A-5

28 3 30.0 5 1 US-07-990-301A-9 Sequence 9, Appli
29 3 30.0 5 1 US-08-584-579-4 Sequence 4, Appli
30 3 30.0 5 1 US-08-676-263-3 Sequence 3, Appli
31 3 30.0 5 1 US-08-406-192-42 Sequence 42, Appli
32 3 30.0 5 1 US-08-749-882A-5 Sequence 5, Appli
33 3 30.0 5 1 US-08-244-415A-6 Sequence 6, Appli
34 3 30.0 5 2 US-08-545-151-42 Sequence 42, Appli
35 3 30.0 5 2 US-08-539-134-5 Sequence 5, Appli
36 3 30.0 5 2 US-08-672-610A-34 Sequence 34, Appli
37 3 30.0 5 2 US-08-672-610A-36 Sequence 36, Appli
38 3 30.0 5 2 US-08-637-759B-303 Sequence 303, App
39 3 30.0 5 2 US-08-422-333-7 Sequence 7, Appli
40 3 30.0 5 2 US-08-747-137-112 Sequence 112, App
41 3 30.0 5 3 US-08-947-965-3 Sequence 3, Appli
42 3 30.0 5 3 US-08-871-355A-303 Sequence 303, App
43 3 30.0 5 3 US-09-138-056-48 Sequence 48, Appli
44 3 30.0 5 3 US-09-138-056-49 Sequence 49, Appli
45 3 30.0 5 3 US-09-138-056-50 Sequence 50, Appli

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55sx
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-12

Query Match 90.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRDSGY 9
DB 2 AEFHRDSGY 10

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RESULT 2
PCT-US94-01712-12
; Sequence 12, Application PCT/US9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-01712-12

Query Match          90.0%; Score 9; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRRHDSGY 9
Db 2 AEFRRHDSGY 10

RESULT 3
US-08-617-267C-36
; Sequence 36, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-617-267C-36

Query Match          50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HDSGY 9
Db 1 HDSGY 5

RESULT 4
US-07-843-949A-8
; Sequence 8, Application US/07843949A
; Patent No. 5340935
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Streuli, Michel
; APPLICANT: Schlossman, Stuart F.
; TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
; TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/843,949A
; FILING DATE: 19920219
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/450,678
; FILING DATE: January 5, 1990
; APPLICATION NUMBER: 07/726,607
; FILING DATE: July 10, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/021003

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-07-843-949A-8

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGYE 10
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DB 1 SGYE 4

RESULT 5
US-08-218-978-8
Sequence 8, Application US/08218978
Patent No. 5837811
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Streuli, Michel
APPLICANT: Schlossman, Stuart F.
TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55sx
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,978
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,949
FILING DATE: February 19, 1992
APPLICATION NUMBER: 07/460,678
FILING DATE: January 5, 1990
APPLICATION NUMBER: 07/726,607
FILING DATE: July 10, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/021003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-218-978-8

Query Match 40.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 SGYE 10
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DB 1 SGYE 4

RESULT 6
US-08-303-861-3
Sequence 3, Application US/08303861
Patent No. 6086902
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20020.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-861-3

Query Match 40.0%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSGY 9
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DB 2 DSGY 5

RESULT 7
US-09-173-941-82
Sequence 82, Application US/09173941
Patent No. 6140081
GENERAL INFORMATION:
APPLICANT: BARBAS, Carlos F.
TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
FILE REFERENCE: NOV0081S
CURRENT APPLICATION NUMBER: US/09/173,941
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 82
LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-82

Query Match          40.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4 RHDS 7
Db  1 RHDS 4

RESULT 8
5177197-3
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 3
; LENGTH: 9
5177197-3

Query Match          40.0%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6 DSGY 9
Db  5 DSGY 8

RESULT 9
US-07-766-351-1
; Sequence 1, Application US/07766351
; Patent No. 5292652
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,351
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
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; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
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; NAME/KEY: Modified-site
; LOCATION: 5
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; OTHER INFORMATION: /note= "Xaa5 can be either Met or Ile"
US-07-766-351-1

Query Match          40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 AEFR 4
Db  7 AEFR 10

RESULT 10
US-08-059-032-1
; Sequence 1, Application US/08059032
; Patent No. 5424205
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower,
; STREET: Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,032
; FILING DATE: 19930507
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William E.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Xaa5
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-08-059-032-1

Query Match          40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEF 4
Db      ||||
       7 AEF 10

RESULT 11
US-08-764-640-119
; Sequence 119, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depirnce, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-119

Query Match          40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEF 4
Db      ||||
       4 AEF 7

RESULT 12
US-08-659-984A-19
; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-00281005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
US-08-659-984A-19

Query Match          40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEF 4
Db      ||||
       7 AEF 10
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RESULT 13
US-08-973-225-119
; Sequence 119, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-08-973-225-119
Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFR 4
Db 4 AEFR 7
RESULT 14
US-09-244-298A-119
; Sequence 119, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.

; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-119
Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFR 4
Db 4 AEFR 7
RESULT 15
US-08-480-332-9
; Sequence 9, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; APPLICANT: Barenholz, Yechezkel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/316,436

Tue Apr 22 16:27:35 2003

;; FILING DATE: 29-SEP-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/035,443
;; FILING DATE: 23-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mohr, Judy M.
;; REGISTRATION NUMBER: 38,563
;; REFERENCE/DOCKET NUMBER: 5325-0115.31
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: Peptide 9, Fig. 13
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..15
US-08-480-332-9

Query Match 40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSGY 9
Db 3 DSGY 6

Search completed: April 21, 2003, 12:43:00
Job time : 11.5 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:40:48 ; Search time 11.5 Seconds
(without alignments)
65.751 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFRRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 31376

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	9	90.0	9	US-09-865-294-69
2	6	60.0	10	US-09-867-847-5
3	5	50.0	5	US-09-972-475-36
4	4	40.0	5	US-09-794-927-72
5	4	40.0	5	US-09-795-847-72
6	4	40.0	5	US-09-794-743-72
7	4	40.0	5	US-09-794-748-72
8	4	40.0	5	US-09-794-925-72
9	4	40.0	5	US-09-681-442-72
10	4	40.0	6	US-09-808-037-7
11	4	40.0	8	US-09-149-718-10
12	4	40.0	10	US-09-795-903A-4
13	4	40.0	10	US-09-795-903A-5
14	4	40.0	10	US-09-794-927-63
15	4	40.0	10	US-09-794-927-64
16	4	40.0	10	US-09-795-847-63
17	4	40.0	10	US-09-795-847-64
18	4	40.0	10	US-09-794-743-63
19	4	40.0	10	US-09-794-743-64

20	4	40.0	10	US-09-794-748-63	Sequence 63, Appl
21	4	40.0	10	US-09-794-748-64	Sequence 64, Appl
22	4	40.0	10	US-09-796-264-4	Sequence 4, Appl
23	4	40.0	10	US-09-796-264-5	Sequence 5, Appl
24	4	40.0	10	US-09-794-925-63	Sequence 63, Appl
25	4	40.0	10	US-09-794-925-64	Sequence 64, Appl
26	4	40.0	10	US-09-681-442-63	Sequence 63, Appl
27	4	40.0	10	US-09-681-442-64	Sequence 64, Appl
28	4	40.0	10	US-09-845-226-4	Sequence 4, Appl
29	4	40.0	10	US-09-845-226-5	Sequence 5, Appl
30	3	30.0	5	US-08-424-550B-364	Sequence 364, App
31	3	30.0	5	US-09-961-721-9	Sequence 9, Appl
32	3	30.0	5	US-10-179-046-15	Sequence 15, Appl
33	3	30.0	5	US-09-910-071-18	Sequence 18, Appl
34	3	30.0	5	US-09-910-071-19	Sequence 19, Appl
35	3	30.0	5	US-09-821-831-72	Sequence 72, Appl
36	3	30.0	5	US-09-748-114-29	Sequence 29, Appl
37	3	30.0	6	US-09-727-963A-21	Sequence 21, Appl
38	3	30.0	6	US-10-059-749-72	Sequence 72, Appl
39	3	30.0	6	US-10-247-488-8	Sequence 8, Appl
40	3	30.0	6	US-10-091-135-89	Sequence 89, Appl
41	3	30.0	6	US-09-880-748-3108	Sequence 3108, Ap
42	3	30.0	6	US-09-952-768-57	Sequence 57, Appl
43	3	30.0	6	US-09-954-697-110	Sequence 110, App
44	3	30.0	6	US-09-982-172-44	Sequence 44, Appl
45	3	30.0	6	US-09-821-831-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

US-09-865-294-69
; Sequence 69, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-69

Query Match 90.0%; Score 9; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRRHDSGY 9
Db 2 AEFRRHDSGY 10

RESULT 2

US-09-867-847-5
; Sequence 5, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

;; PRIOR APPLICATION NUMBER: 60/168,594
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: 09/724,842
;; PRIOR FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
;; OTHER INFORMATION: or peptidomimetics
US-09-867-847-5

Query Match 60.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRD 6
Db 2 AEPHRD 7

RESULT 3
US-09-972-475-36
;; Sequence 36, Application US/09972475
;; Patent No. US20020098173A1
;; GENERAL INFORMATION:
;; APPLICANT: Findels, Mark A. et al.
;; TITLE OF INVENTION: Modulators of Amyloid Aggregation
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,475
FILING DATE: 04-Oct-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,267
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-972-475-36

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 HDSGY 9
Db 1 HDSGY 5

RESULT 4
US-09-794-927-72
;; Sequence 72, Application US/09794927
;; Patent No. US20010016324A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrichson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang

;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;; TITLE OF INVENTION: USES
;; FILE REFERENCE: 28341/6280FG
;; CURRENT APPLICATION NUMBER: US/09/794,927
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 72
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
Db 2 AEFR 5

RESULT 5
US-09-795-847-72
;; Sequence 72, Application US/09795847
;; Patent No. US20010018208A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrichson, Robert L.
;; APPLICANT: Parodi, Luis A.

;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;; TITLE OF INVENTION: USES
;; FILE REFERENCE: 28341/6280DE
;; CURRENT APPLICATION NUMBER: US/09/795,847
;; CURRENT FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
| | | |
Db 2 AEFR 5

RESULT 6
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
| | | |
Db 2 AEFR 5

RESULT 7
US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1

; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Query Match 40.0%; Score 4; DB 10; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
| | | |
Db 2 AEFR 5

RESULT 8
US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
Db 2 AEFR 5

RESULT 9

US-09-681-442-72

; Sequence 72, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681.442

; CURRENT FILING DATE: 2001-04-05

; PRIOR FILING DATE: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 72

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-681-442-72

Query Match 40.0%; Score 4; DB 10; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
Db 2 AEFR 5

RESULT 10

US-09-808-037-7

; Sequence 7, Application US/09808037

; Patent No. US20020052311A1

; GENERAL INFORMATION:

; APPLICANT: SOLOMON, Beka

; APPLICANT: HANAN, Eliat

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS

; CURRENT APPLICATION NUMBER: 2001-03-15

; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 09/629,971

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 09/473,653

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: US 60/152,417

; PRIOR FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-09-808-037-7

Query Match 40.0%; Score 4; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRH 5
Db 3 EFRH 6

RESULT 11

US-09-149-718-10

; Sequence 10, Application US/09149718

; Patent No. US20020104104A1

; GENERAL INFORMATION:

; APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,

; APPLICANT: Peter A. Seubert, and Russell E. Rydel

; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease

; TITLE OF INVENTION: Therapeutics Using Transgenic Animal Models

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; STREET: 1201 West Peachtree Street

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/149,718

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,487

; FILING DATE:

; APPLICATION NUMBER: 08/480,653

; FILING DATE: June 7, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: ANS101CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794

; TELEFAX: (404)-873-8795

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-149-718-10

Query Match 40.0%; Score 4; DB 10; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
Db 11111

Db 2 AEFR 5

RESULT 12

US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Koelsch, Gerald
; APPLICANT: Lin, Xinli
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match 40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
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|
|
|
DB 7 AEFR 10

RESULT 13

US-09-795-903A-5
; Sequence 5, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT

Query Match 40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-795-903A-5

Query Match 40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
|
|
|
|
DB 7 AEFR 10

RESULT 14

US-09-794-927-63
; Sequence 63, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-63

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
|
|
|
|
DB 7 AEFR 10

RESULT 15

US-09-794-927-64
; Sequence 64, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-64

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Query Match      40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEFR 4
Db 7 AEFR 10

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Search completed: April 21, 2003, 12:43:30
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:35 ; Search time 10 Seconds
(without alignments)
29,423 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAEFRHDSG 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA: *
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	9	90.0	10	1	US-08-371-930-12
2	9	90.0	10	5	PCT-US94-01712-12
3	6	60.0	10	4	US-09-548-372D-64
4	6	60.0	10	4	US-09-548-367D-64
5	5	50.0	5	2	US-08-422-333-7
6	5	50.0	5	6	5187153-6
7	5	50.0	5	6	5220013-6
8	5	50.0	5	6	5223482-6
9	5	50.0	7	2	US-08-792-553-10
10	5	50.0	8	4	US-09-548-372D-67
11	5	50.0	8	4	US-09-548-367D-67
12	5	50.0	9	3	US-08-802-981-221
13	5	50.0	9	4	US-09-294-987-6
14	5	50.0	10	1	US-07-766-351-1
15	5	50.0	10	1	US-08-059-032-1
16	5	50.0	10	2	US-08-025-321C-1
17	5	50.0	10	2	US-08-659-984A-19
18	5	50.0	10	4	US-08-660-531-19
19	5	50.0	10	4	US-09-548-372D-63
20	5	50.0	10	4	US-09-548-367D-63
21	5	50.0	10	5	PCT-US91-07290-1
22	4	40.0	4	4	US-09-513-783A-92
23	4	40.0	5	4	US-08-617-267C-36
24	4	40.0	7	1	US-08-136-743B-33
25	4	40.0	7	1	US-08-136-743B-35
26	4	40.0	7	1	US-08-136-743B-56
27	4	40.0	7	3	US-09-040-216-29

28 4 40.0 7 4 US-09-173-941-82 Sequence 82, Appl
29 4 40.0 9 3 US-08-802-981-219 Sequence 219, App
30 4 40.0 9 3 US-08-802-981-220 Sequence 220, App
31 4 40.0 10 2 US-08-764-640-119 Sequence 119, App
32 4 40.0 10 3 US-08-973-225-119 Sequence 119, App
33 4 40.0 10 3 US-09-244-298A-119 Sequence 119, App
34 4 40.0 10 4 US-09-516-704-119 Sequence 119, App
35 4 40.0 10 4 US-09-549-090-119 Sequence 119, App
36 3 30.0 4 1 US-07-750-330-3 Sequence 3, Appli
37 3 30.0 4 1 US-07-750-330-4 Sequence 4, Appli
38 3 30.0 4 1 US-07-780-790A-9 Sequence 9, Appli
39 3 30.0 4 1 US-08-022-411-5 Sequence 5, Appli
40 3 30.0 4 2 US-08-441-871-2 Sequence 2, Appli
41 3 30.0 4 2 US-08-672-610A-33 Sequence 33, Appli
42 3 30.0 4 4 US-09-117-121-1 Sequence 1, Appli
43 3 30.0 4 4 US-09-187-859-114 Sequence 114, App
44 3 30.0 4 4 US-09-187-859-115 Sequence 115, App
45 3 30.0 4 4 US-09-187-859-169 Sequence 169, App

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-12

Query Match 90.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAEFRHDSG 10
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Db 1 DAEFRHDSG 9

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RESULT 2
PCT-US94-01712-12
; Sequence 12, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-01712-12

Query Match 90.0%; Score 9; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAEFRHDSG 10
Db 1 DAEFRHDSG 9

RESULT 3
US-09-548-372D-64
; Sequence 64, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 60.0%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 4
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match 60.0%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 5
US-08-422-333-7
; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIOS, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-7

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 1 MDAEF 5

RESULT 6
5187153-6
;Patent No. 5187153
; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6:
; LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 1 MDAEF 5

RESULT 7
5220013-6
;Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION

OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6:
; LENGTH: 5
5220013-6

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 1 MDAEF 5

RESULT 8
5223482-6
;Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6:
; LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 1 MDAEF 5

RESULT 9
US-08-792-553-10
; Sequence 10, Application US/08792553
; Patent No. 5981200
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Heim, Roger
; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 1 MDAEF 5

STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-792-553-10

Query Match 50.0%; Score 5; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 3 MDAEF 7

RESULT 10
US-09-548-372D-67
; Sequence 67, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-372D-67

Query Match 50.0%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5

Db 4 MDAEF 8

RESULT 11
US-09-548-367D-67
; Sequence 67, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-367D-67

Query Match 50.0%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
Db 4 MDAEF 8

RESULT 12
US-08-802-981-221
; Sequence 221, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-221

Query Match 50.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEF 5
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DB 5 MDAEF 9

RESULT 13
US-09-294-987-6
Sequence 6, Application US/09294987
Patent No. 6313268
GENERAL INFORMATION:
APPLICANT: Hook, Vivian Y.H.
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
FILE REFERENCE: P-AS 3515
CURRENT APPLICATION NUMBER: US/09/294,987
CURRENT FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: US 09/173,887
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: mammalian
US-09-294-987-6

Query Match 50.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEF 5
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DB 5 MDAEF 9

RESULT 14
US-07-766-351-1
Sequence 1, Application US/07766351
Patent No. 5292652
GENERAL INFORMATION:
APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConlogue, Lisa C.
APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Athena Neurosciences, Inc.
STREET: 800F Gateway Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,351
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
REFERENCE/DOCKET NUMBER: 17796-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= Xaa4
OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
FEATURE:
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LOCATION: 5
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US-07-766-351-1

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Best Local Similarity 100.0%; Pred. No. 4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAEFR 6
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DB 6 DAEFR 10

RESULT 15
US-08-059-032-1
Sequence 1, Application US/08059032
Patent No. 5424205
GENERAL INFORMATION:
APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConlogue, Lisa C.
APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Street Tower,
STREET: Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,032
FILING DATE: 19930507
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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; NAME: Smith, William E.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
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; US-08-059-032-1
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 DAEFR 6
Db 6 DAEFR 10
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Job time : 11 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:05 ; Search time 11.3333 Seconds
(without alignments)
66.718 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAEFRHDSG 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 33473

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	10	9	US-09-865-294-69
2	7	70.0	7	10	US-09-867-847-5
3	6	60.0	10	9	US-09-795-903A-4
4	6	60.0	10	10	US-09-794-927-64
5	6	60.0	10	10	US-09-795-847-64
6	6	60.0	10	10	US-09-794-743-64
7	6	60.0	10	10	US-09-794-748-64
8	6	60.0	10	10	US-09-796-264-4
9	6	60.0	10	10	US-09-794-925-64
10	6	60.0	10	10	US-09-681-442-64
11	6	60.0	10	10	US-09-845-226-4
12	5	50.0	5	10	US-09-794-927-72
13	5	50.0	5	10	US-09-795-847-72
14	5	50.0	5	10	US-09-794-743-72
15	5	50.0	5	10	US-09-794-748-72
16	5	50.0	5	10	US-09-794-925-72
17	5	50.0	5	10	US-09-681-442-72
18	5	50.0	7	9	US-10-057-505-10
19	5	50.0	8	10	US-09-794-927-67

20	5	50.0	8	10	US-09-795-847-67	Sequence 67, Appl
21	5	50.0	8	10	US-09-794-743-67	Sequence 67, Appl
22	5	50.0	8	10	US-09-794-748-67	Sequence 67, Appl
23	5	50.0	8	10	US-09-794-925-67	Sequence 67, Appl
24	5	50.0	8	10	US-09-681-442-67	Sequence 67, Appl
25	5	50.0	8	10	US-09-149-718-10	Sequence 10, Appl
26	5	50.0	9	12	US-10-016-717-6	Sequence 6, Appl
27	5	50.0	10	9	US-09-795-903A-5	Sequence 5, Appl
28	5	50.0	10	10	US-09-794-927-63	Sequence 63, Appl
29	5	50.0	10	10	US-09-795-847-63	Sequence 63, Appl
30	5	50.0	10	10	US-09-794-743-63	Sequence 63, Appl
31	5	50.0	10	10	US-09-794-748-63	Sequence 63, Appl
32	5	50.0	10	10	US-09-796-264-5	Sequence 5, Appl
33	5	50.0	10	10	US-09-794-925-63	Sequence 63, Appl
34	5	50.0	10	10	US-09-681-442-63	Sequence 63, Appl
35	5	50.0	10	10	US-09-845-226-5	Sequence 5, Appl
36	4	40.0	4	10	US-09-808-037-1	Sequence 1, Appl
37	4	40.0	5	10	US-09-972-475-36	Sequence 36, Appl
38	4	40.0	6	10	US-09-808-037-7	Sequence 7, Appl
39	4	40.0	9	10	US-09-896-874-8	Sequence 8, Appl
40	4	40.0	9	10	US-09-896-139-8	Sequence 8, Appl
41	4	40.0	9	10	US-09-895-843-8	Sequence 8, Appl
42	3	30.0	4	9	US-10-029-191-10	Sequence 10, Appl
43	3	30.0	4	9	US-10-091-135-90	Sequence 90, Appl
44	3	30.0	4	9	US-09-848-616-88	Sequence 88, Appl
45	3	30.0	4	10	US-09-916-230-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-69
; Sequence 69, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-69

Query Match 90.0%; Score 9; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAEFRHDSG 10
Db 1 DAEFRHDSG 9

RESULT 2
US-09-867-847-5
; Sequence 5, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-5

Query Match 70.0%; Score 7; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DAEFRHD 8
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Db 1 DAEFRHD 7

RESULT 3
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Kolsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match 60.0%; Score 6; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAEFR 6
| | | | |
Db 5 MDAEFR 10

RESULT 4
US-09-794-927-64
; Sequence 64, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAEFR 6
| | | | |
Db 5 MDAEFR 10

RESULT 5
US-09-795-847-64
; Sequence 64, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
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Db 5 MDAEFR 10

RESULT 6

US-09-794-743-64
; Sequence 64, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
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Db 5 MDAEFR 10

RESULT 7

US-09-794-748-64
; Sequence 64, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
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Db 5 MDAEFR 10

RESULT 8

US-09-796-264-4
; Sequence 4, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-796-264-4

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
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Db 5 MDAEFR 10

RESULT 9
US-09-794-925-64
; Sequence 64, Application US/09794925
; Patent No. US20020064819A1

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; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/6280FI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-64

Query Match          60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
DB 5 MDAEFR 10

RESULT 10
US-09-681-442-64
; Sequence 64, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-64

Query Match          60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
DB 5 MDAEFR 10

RESULT 11
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4

Query Match          60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
DB 5 MDAEFR 10

RESULT 12
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72
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US-09-681-442-64
Query Match          60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
DB 5 MDAEFR 10

RESULT 11
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
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; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4

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Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
DB 5 MDAEFR 10

RESULT 12
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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US-09-794-927-72
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 DAEFR 5
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RESULT 13
US-09-795-847-72
; Sequence 72, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DAEFR 6
Db      1 DAEFR 5
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RESULT 14
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; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
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; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DAEFR 6
Db      1 DAEFR 5
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RESULT 15
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; Sequence 72, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

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Qy	2	DAEFR 6
Db	1	DAEFR 5

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Job time : 11.3333 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:35 ; Search time 10 Seconds
(without alignments)
29.423 Million cell updates/sec

Title: US-09-580-018-9
Perfect score: 10
Sequence: 1 DAEFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

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Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	5	50.0	10	1	US-07-766-351-1
5	5	50.0	10	1	US-08-059-032-1
6	5	50.0	10	2	US-08-659-984A-19
7	5	50.0	10	4	US-08-660-531-19
8	5	50.0	10	4	US-09-548-372D-63
9	5	50.0	10	4	US-09-548-372D-64
10	5	50.0	10	4	US-09-548-367D-63
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12	5	50.0	10	5	PCT-US91-07290-1
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15	4	40.0	5	6	5187153-6
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17	4	40.0	5	6	5223482-6
18	4	40.0	7	1	US-08-136-743B-33
19	4	40.0	7	1	US-08-136-743B-35
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21	4	40.0	7	2	US-08-792-553-10
22	4	40.0	7	3	US-09-040-216-29
23	4	40.0	7	3	US-08-303-861-3
24	4	40.0	7	4	US-09-173-941-82
25	4	40.0	8	4	US-09-548-372D-67
26	4	40.0	8	4	US-09-548-367D-67
27	4	40.0	9	3	US-08-802-981-219

28 4 40.0 9 3 US-08-802-981-220 Sequence 220, App
29 4 40.0 9 3 US-08-802-981-221 Sequence 221, App
30 4 40.0 9 4 US-09-294-987-6 Patent No. 5177197
31 4 40.0 9 6 5177197-3
32 4 40.0 10 2 US-08-025-321C-1 Sequence 1, Appli
33 4 40.0 10 2 US-08-764-640-119 Sequence 119, App
34 4 40.0 10 3 US-08-973-225-119 Sequence 119, App
35 4 40.0 10 3 US-09-244-298A-119 Sequence 119, App
36 4 40.0 10 4 US-08-480-332-9 Sequence 119, App
37 4 40.0 10 4 US-09-516-704-119 Sequence 119, App
38 4 40.0 10 4 US-09-549-090-119 Sequence 119, App
39 3 30.0 4 1 US-07-750-330-3 Sequence 3, Appli
40 3 30.0 4 1 US-07-750-330-4 Sequence 4, Appli
41 3 30.0 4 1 US-07-780-790A-9 Sequence 9, Appli
42 3 30.0 4 1 US-08-022-411-5 Sequence 2, Appli
43 3 30.0 4 2 US-08-441-871-2 Sequence 2, Appli
44 3 30.0 4 2 US-08-672-610A-33 Sequence 33, Appli
45 3 30.0 4 3 US-09-138-056-58 Sequence 58, Appli

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55sx
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-12

Query Match 100.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGY 10
DB 1 DAEFRHDSGY 10

RESULT 2
PCT-US94-01712-12
; Sequence 12, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-01712-12
Query Match 100.0%; Score 10; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGY 10
Db 1 DAEFRHDSGY 10
RESULT 3
US-08-617-267C-36
; Sequence 36, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-36
Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 HD SGY 10
Db 1 HD SGY 5
RESULT 4
US-07-766-351-1
; Sequence 1, Application US/07766351
; Patent No. 5292652
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,351
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /label= Xaa4
;   OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
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;   NAME/KEY: Modified-site
;   LOCATION: 5
;   OTHER INFORMATION: /label= Xaa5
;   OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
; US-07-766-351-1
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; Query Match          50.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 5.1;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DAEFR 5
; Db 6 DAEFR 10
;
; RESULT 5
; US-08-059-032-1
; Sequence 1, Application US/08059032
; Patent No. 5424205
; GENERAL INFORMATION:
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Seubert, Peter A.
;   APPLICANT: Dovey, Harry F.
;   APPLICANT: McConlogue, Lisa C.
;   APPLICANT: Little, Sheila P.
;   APPLICANT: Johnstone, Edward M.
;   TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Townsend and Townsend Khourie and Crew
;     STREET: One Market Plaza, Steuart Street Tower,
;     STREET: Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/059,032
;     FILING DATE: 19930507
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William E.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-10
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 326-2400
;     TELEFAX: (415) 326-2422
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /label= Xaa4
;   OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 5
;   OTHER INFORMATION: /label= Xaa5
;   OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
; US-08-059-032-1
;
; Query Match          50.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 5.1;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DAEFR 5
; Db 6 DAEFR 10
;
; RESULT 6
; US-08-659-984A-19
; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Jacobson-Croak, Kirsten L.
;   TITLE OF INVENTION: Assays for Detecting Beta-Secretase
;   TITLE OF INVENTION: Inhibition
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Ctr., 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/659,984A
;     FILING DATE: 07-JUN-1996
;     CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/485,152
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Heslin, James M.
;     REGISTRATION NUMBER: 29,541
;     REFERENCE/DOCKET NUMBER: 15270-0028100S
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: Region
;       LOCATION: one-of(1)
;     OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
; US-08-659-984A-19
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Query Match 50.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 6 DAEFR 10

RESULT 7
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-0022100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
US-08-660-531-19

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 6 DAEFR 10

RESULT 8
US-09-548-372D-63
; Sequence 63, Application US/09548372D
; Patent No. 6420534

; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-63

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 6 DAEFR 10

RESULT 9
US-09-548-372D-64
; Sequence 64, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 6 DAEFR 10

RESULT 10

US-09-548-367D-63
; Sequence 63, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-63

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
|||||
Db 6 DAEFR 10

RESULT 11
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
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Db 6 DAEFR 10

RESULT 12
PCT-US91-07290-1
; Sequence 1, Application PC/TUS9107290
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07290
; FILING DATE: 19911004
; CLASSIFICATION: 435
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Xaa5
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
PCT-US91-07290-1

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Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
|||||
Db 6 DAEFR 10

RESULT 13
US-09-513-783A-92
; Sequence 92, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.

APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: b-Secretase
OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-92

Query Match 40.0%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEF 4
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Db 1 DAEF 4

RESULT 14
US-08-422-333-7
Sequence 7, Application US/08422333
Patent No. 5912410
GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-7

Query Match 40.0%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEF 4
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Db 2 DAEF 5

RESULT 15
5187153-6
Patent No. 5187153
APPLICANT: CORDELL, BARBARA SCHILLING, JAMES W., KATUNUMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
AMYLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 6;
LENGTH: 5
5187153-6

Query Match 40.0%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEF 4
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Db 2 DAEF 5

Search completed: April 21, 2003, 12:12:56
Job time : 10 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:05 ; Search time 11.3333 Seconds
(without alignments)
66.718 Million cell updates/sec

Title: US-09-580-018-9

Perfect score: 10

Sequence: 1 DAEFRHDSGY 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 33473

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

Published Applications_AA:*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	10	100.0	10	9	US-09-865-294-69
2	7	70.0	7	10	US-09-867-847-5
3	5	50.0	5	10	US-09-794-927-72
4	5	50.0	5	10	US-09-795-847-72
5	5	50.0	5	10	US-09-794-743-72
6	5	50.0	5	10	US-09-794-748-72
7	5	50.0	5	10	US-09-794-925-63
8	5	50.0	5	10	US-09-681-442-72
9	5	50.0	5	10	US-09-792-475-36
10	5	50.0	8	10	US-09-149-718-10
11	5	50.0	10	9	US-09-795-903A-4
12	5	50.0	10	9	US-09-795-903A-5
13	5	50.0	10	10	US-09-794-927-63
14	5	50.0	10	10	US-09-794-927-64
15	5	50.0	10	10	US-09-795-847-63
16	5	50.0	10	10	US-09-795-847-64
17	5	50.0	10	10	US-09-794-743-63
18	5	50.0	10	10	US-09-794-743-64
19	5	50.0	10	10	US-09-794-748-63

Sequence 64, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 63, Appl
Sequence 64, Appl
Sequence 63, Appl
Sequence 64, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 10, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 90, Appl
Sequence 88, Appl
Sequence 19, Appl

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22 5 50.0 10 10 US-09-796-264-5
23 5 50.0 10 10 US-09-794-925-63
24 5 50.0 10 10 US-09-794-925-64
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26 5 50.0 10 10 US-09-681-442-64
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28 5 50.0 10 10 US-09-845-226-5
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30 4 40.0 6 10 US-09-808-037-7
31 4 40.0 7 9 US-10-057-505-10
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35 4 40.0 8 10 US-09-794-748-67
36 4 40.0 8 10 US-09-794-925-67
37 4 40.0 8 10 US-09-681-442-67
38 4 40.0 9 10 US-09-896-874-8
39 4 40.0 9 10 US-09-896-139-8
40 4 40.0 9 10 US-09-895-843-8
41 4 40.0 9 12 US-10-016-717-6
42 3 30.0 4 9 US-10-029-191-10
43 3 30.0 4 9 US-10-091-135-90
44 3 30.0 4 9 US-09-848-616-88
45 3 30.0 4 10 US-09-916-230-19

ALIGNMENTS

RESULT 1

US-09-865-294-69

; Sequence 69, Application US/09865294

; Publication No. US20030068325A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease

; FILE REFERENCE: 1151-4167

; CURRENT APPLICATION NUMBER: US/09/865,294

; CURRENT FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 69

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-865-294-69

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Best Local Similarity 100.0%; Score 10; DB 9; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGY 10

Db 1 DAEFRHDSGY 10

RESULT 2

US-09-867-847-5

; Sequence 5, Application US/09867847

; Patent No. US20020094335A1

; GENERAL INFORMATION:

; APPLICANT: Chalfour, Robert

; APPLICANT: Hebert, Lise

; APPLICANT: Kong, Xiang

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE AND AMYLOID RELATED DISEASES

; FILE REFERENCE: 14445-501 CIP

; CURRENT APPLICATION NUMBER: US/09/867,847

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-5

Query Match 70.0%; Score 7; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHD 7
| | | | |
DB 1 DAEFRHD 7

RESULT 3
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | |
DB 1 DAEFR 5

RESULT 4
US-09-795-847-72
; Sequence 72, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
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DB 1 DAEFR 5

RESULT 5
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAEFR 5

RESULT 5
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
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DB 1 DAEFR 5

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US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | |
DB 1 DAEFR 5

RESULT 5
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | | |
Db 1 DAEFR 5

RESULT 6

US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | | |
Db 1 DAEFR 5

RESULT 7

US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | | |
Db 1 DAEFR 5

RESULT 8

US-09-681-442-72
; Sequence 72, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
| | | | |
Db 1 DAEFR 5

RESULT 9

US-09-972-475-36
; Sequence 36, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Flindeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-972-475-36

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HDSGY 10
Db 1 HDSGY 5

RESULT 10

US-09-149-718-10
; Sequence 10, Application US/09149718
; Patent No. US20020104104A1
; GENERAL INFORMATION:
; APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
; APPLICANT: Peter A. Seubert, and Russell E. Rydel
; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA

Query Match 50.0%; Score 5; DB 9; Length 10;

ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,487
; FILING DATE:
; APPLICATION NUMBER: 08/480,653
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: ANS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-149-718-10

Query Match 50.0%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 1 DAEFR 5

RESULT 11

US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PET
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match 50.0%; Score 5; DB 9; Length 10;

; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-63

Query Match 50.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

Search completed: April 21, 2003, 12:13:36
Job time : 12.3333 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:50 ; Search time 22 Seconds
(without alignments)
93.658 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFRRHDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	8	13 Q9PS69	Q9PS69 gallus gall
2	3	30.0	10	6 Q9TU33	Q9TU33 canis fami
3	3	30.0	10	10 P81899	P81899 prunus dulc
4	3	30.0	10	12 Q9JIG8	Q9JIG8 tt virus. o
5	2	20.0	7	2 Q47477	Q47477 escherichia
6	2	20.0	7	4 Q15897	Q15897 homo sapien
7	2	20.0	7	6 Q28742	Q28742 oryctolagus
8	2	20.0	7	8 Q98866	Q98866 spinacia ol
9	2	20.0	8	2 Q68485	Q68485 klebsiella
10	2	20.0	8	2 Q9X3K1	Q9X3K1 prochloroco
11	2	20.0	8	2 Q9S6D5	Q9S6D5 escherichia
12	2	20.0	8	2 P72221	P72221 pseudomonas
13	2	20.0	8	2 Q9R7I2	Q9R7I2 escherichia
14	2	20.0	8	2 Q9R5R2	Q9R5R2 shigella dy
15	2	20.0	8	2 Q9R3X0	Q9R3X0 planktothri
16	2	20.0	8	2 Q9R5L7	Q9R5L7 clostridium

17	2	20.0	8	2	Q8RSR3	Q8RSR3 lactobacill
18	2	20.0	8	4	Q9UJ50	Q9UJ50 homo sapien
19	2	20.0	8	4	Q15901	Q15901 homo sapien
20	2	20.0	8	4	Q9Y4J4	Q9Y4J4 homo sapien
21	2	20.0	8	4	Q16428	Q16428 homo sapien
22	2	20.0	8	4	Q60773	Q60773 homo sapien
23	2	20.0	8	5	Q94623	Q94623 manduca sex
24	2	20.0	8	5	Q9TWH6	Q9TWH6 perinereis
25	2	20.0	8	6	Q9MYL5	Q9MYL5 pongo pygma
26	2	20.0	8	6	Q9GMH3	Q9GMH3 lagenorhync
27	2	20.0	8	6	Q28866	Q28866 megaptera n
28	2	20.0	8	6	Q8WNS1	Q8WNS1 bos taurus
29	2	20.0	8	6	Q9BFC3	Q9BFC3 didelphis m
30	2	20.0	8	6	Q9BFC2	Q9BFC2 macropus eu
31	2	20.0	8	6	Q9BFC1	Q9BFC1 choleopus h
32	2	20.0	8	6	Q9BFC0	Q9BFC0 choleopus d
33	2	20.0	8	6	Q9BFB9	Q9BFB9 euphractus
34	2	20.0	8	6	Q9BFB8	Q9BFB8 chaetophrac
35	2	20.0	8	6	Q9BFB7	Q9BFB7 tamandua te
36	2	20.0	8	6	Q9BFB6	Q9BFB6 myrmecophag
37	2	20.0	8	6	Q9BFB5	Q9BFB5 erinaceus c
38	2	20.0	8	6	Q9BFB4	Q9BFB4 talpa alta
39	2	20.0	8	6	Q9BFB3	Q9BFB3 condylura c
40	2	20.0	8	6	Q9BFB2	Q9BFB2 sorex arane
41	2	20.0	8	6	Q9BFB1	Q9BFB1 echinops te
42	2	20.0	8	6	Q9BFB0	Q9BFB0 trichechus
43	2	20.0	8	6	Q9BFA9	Q9BFA9 procavia ca
44	2	20.0	8	6	Q9BFA8	Q9BFA8 loxodonta a
45	2	20.0	8	6	Q9BFA7	Q9BFA7 macroscllid

ALIGNMENTS

RESULT 1

Q9PS69 ID Q9PS69 PRELIMINARY; PRT; 8 AA.
AC Q9PS69;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;

Query Match 30.0%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DSG 8
Db 2 DSG 4

RESULT 2

Q9TU33 ID Q9TU33 PRELIMINARY; PRT; 10 AA.
AC Q9TU33;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

```

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BRCA1. (Fragment).
CN Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20154965; PubMed=10690375;
RA Gray I.S., Yuzbaslyan-Gurkan V.;
RT "A single nucleotide (T->G) polymorphism within intron 23 of the
RL canine BRCA1 gene.";
RL Anim. Genet. 31:76-77(2000).
DR EMBL; AF159258; AAD56289.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DSG 8
Db 6 DSG 8

RESULT 3
P81899 PRELIMINARY; PRT; 10 AA.
AC P81899;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large
DE chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX PubMed=9523720;
RA Altman F., Paschinger K., Dalik T., Vorauer K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT amidase A and its N-glycans.";
RL Eur. J. Biochem. 252:118-123(1998).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -1- MASS SPECTROMETRY: MW=54182; METHOD=MALDI-MS.
KW Hydrolase; Glycoprotein.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGY 9
Db 3 SGY 5

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RESULT 4
Q9JIG8 PRELIMINARY; PRT; 10 AA.
AC Q9JIG8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -.
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEF 3
Db 2 AEF 4

RESULT 5
Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDDBD1D80 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2
Db 1 AE 2

RESULT 6
Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (Tremblrel. 01, Created)

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DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE (clone XP6A11A) (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=PLACENTA;
 RC Lee C.-C., Yardeni A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: L32077; AAA73887.1; -.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

 Query Match 20.0%; Score 2; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AE 2
 DB 5 AE 6

 RESULT 7
 Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL: K01698; AAA31415.1; -.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1B59326B0 CRC64;

 Query Match 20.0%; Score 2; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 HD 6
 DB 4 HD 5

 RESULT 8
 Q98866 PRELIMINARY; PRT; 7 AA.
 AC Q98866;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE Cytochrome b/f subunit IV (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OC NCBI_TaxID=3562;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=86120353; PubMed=3003688;
 RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
 RT protein S11 and RNA polymerase alpha-subunit.";
 RL Nucleic Acids Res. 14:1029-1044(1986).
 DR EMBL: X03496; CAA27215.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 7 AA; 907 MW; 644729D77409C420 CRC64;
 SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

 Query Match 20.0%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 FR 4
 DB 2 FR 3

 RESULT 9
 Q58485 PRELIMINARY; PRT; 8 AA.
 AC Q58485;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
 GN AADAI.
 OS Klebsiella pneumoniae.
 OG Plasmid pQ1000.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella
 OC NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=98287600; PubMed=9624504;
 RA Centron D., Roy P.H.;
 RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
 RT aac(6')-Iq from the integron of a natural multiresistance plasmid.";
 RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
 DR EMBL: AF047556; AAC25501.1; -.
 KW Plasmid; Transferase.
 FT NON_TER 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

 Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AE 2
 DB 3 AE 4

 RESULT 10
 Q9X3K1 PRELIMINARY; PRT; 8 AA.
 AC Q9X3K1;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE Cytochrome b (Fragment).
 GN PRTB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.

```

OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070193; AAD23233.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
DB 5 SG 6

RESULT 11
Q9S6D5 PRELIMINARY; PRT; 8 AA.
ID Q9S6D5
AC Q9S6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative IS30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Rahn A., Drummelsmith J., Whitfield C.;
RC MEDLINE=9919477; PubMed=10094716;
RX STRAIN=A295B;
RT "Conserved organization in the cps gene clusters for expression of
RT Escherichia coli group 1 k antigens: relationship to the colanic acid
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 7 AE 8

RESULT 12
P72221 PRELIMINARY; PRT; 8 AA.
ID P72221
AC P72221;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alginatase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=OS-ALG-9;
RX MEDLINE=93329366; PubMed=83361113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an alginatase lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38469; BAA21704.1; -.
KW Lyase..
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 7 AE 8

RESULT 13
Q9R7T2 PRELIMINARY; PRT; 8 AA.
ID Q9R7T2
AC Q9R7T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN YQFG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba T., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996).
DR EMBL; D90705; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 5 AE 6

RESULT 14
Q9R5R2 PRELIMINARY; PRT; 8 AA.
ID Q9R5R2
AC Q9R5R2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 31,000 DA product of ORF8 (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=622;

```

```
RN SEQUENCE.
RP MEDLINE=92085268; PubMed=1660923;
RA Polard P., Prere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 902 MW; FE2DCAF586AE336 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GY 9
Db 4 GY 5

RESULT 15
Q9R3X0
ID Q9R3X0 PRELIMINARY; PRT; 8 AA.
AC Q9R3X0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Planktothrix rubescens.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
OX NCBI_TaxID=59512;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, AND BC-PLA 9303;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
RT "The diversity of gas vesicle genes in Planktothrix rubescens from
Lake Zurich.";
RL Microbiology 145:2757-2768(1999).
DR EMBL; AJ132249; CAB59537.1; -.
DR EMBL; AJ132248; CAB59534.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 957 MW; 33D1AAA685BB19CB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EF 3
Db 1 EF 2

Search completed: April 21, 2003, 12:11:40
Job time : 23 secs
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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	3	30.0	5	2	A26830		mitosis inhibiting
2	3	30.0	8	2	S78036		ribosomal protein
3	3	30.0	10	2	A59272		peptide-M4-(N-acet
4	3	30.0	10	2	PT0243		Ig heavy chain CRD
5	3	30.0	10	2	PT0215		T-cell receptor be
6	3	30.0	10	2	PH0900		T-cell receptor be
7	2	20.0	3	3	PT0571		T-cell receptor be
8	2	20.0	4	2	S09478		globulin IV alpha
9	2	20.0	4	2	PT0633		T-cell receptor be
10	2	20.0	4	2	PT0711		T-cell receptor be
11	2	20.0	4	2	PT0698		T-cell receptor be
12	2	20.0	4	2	PT0677		T-cell receptor be
13	2	20.0	4	2	PT0705		T-cell receptor be
14	2	20.0	4	2	PT0675		T-cell receptor be
15	2	20.0	4	2	PT0566		T-cell receptor be
16	2	20.0	5	2	A41225		copper resistance
17	2	20.0	5	2	B41225		copper resistance
18	2	20.0	5	2	D60274		major protein anti
19	2	20.0	5	2	B37988		acid proteinase li
20	2	20.0	5	2	A44692		fulcins - giant Af
21	2	20.0	5	2	JT0520		Ig kappa chain V-I
22	2	20.0	5	2	D44823		synaptosomal-assoc
23	2	20.0	5	2	PT0513		T-cell receptor be
24	2	20.0	5	2	PT0600		T-cell receptor be
25	2	20.0	5	2	PT0608		T-cell receptor be
26	2	20.0	5	2	PT0669		T-cell receptor be
27	2	20.0	5	2	PT0553		T-cell receptor be
28	2	20.0	5	2	PT0538		T-cell receptor be
29	2	20.0	5	2	PT0540		T-cell receptor be

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain
 N;Alternate names: peptide N-glycosidase
 C;Species: Prunus dulcis var. sativa (sweet almond)
 C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
 A;Accession: A59272
 R;Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
 Eur. J. Biochem. 252, 118-123, 1998
 A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
 A;Reference number: A59272; MUID:98181894; PMID:9523720
 A;Accession: A59272
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <ALT>
 C;Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGY 9
 |||
 Db 3 SGY 5

RESULT 4

PT0243
 Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0243
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0243
 A;Molecule type: DNA
 A;Residues: 1-10 <YAN>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGY 9
 |||
 Db 7 SGY 9

RESULT 5

PT0215
 T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C;Accession: PT0215
 R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
 A;Reference number: PT0209; MUID:91217621; PMID:1902501
 A;Accession: PT0215
 A;Molecule type: mRNA
 A;Residues: 1-10 <NAK>
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GYE 10
 |||
 Db 5 GYE 7

RESULT 6

PH0900
 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0900
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0900
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Experimental source: myelin basic protein-immunized T-cell
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSG 8
 |||
 Db 5 DSG 7

RESULT 7

PT0571
 T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: PT0571
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0571
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-3 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
 ||
 Db 2 SG 3

RESULT 8

S09478
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N;Alternate names: 11S globulin alpha subunit gamma chain
 C;Species: Cucurbita sp. (cucurbit)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C;Accession: S09478
 R;Ohmiya, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic a
 A;Reference number: S09066
 A;Accession: S09478
 A;Molecule type: protein
 A;Residues: 1-4 <OHM>

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GY 9
 ||
 Db 3 GY 4

RESULT 9
PT0633
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0633
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0633
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE2>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

RESULT 10
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0607

A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE1>
A:Experimental source: newborn thymus, strain BALB/c, 120-2J
A:Accession: PT0674

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A:Accession: PT0678
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE3>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A:Accession: PT0570
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE4>

A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A:Accession: PT0711

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE5>

A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

RESULT 11
PT0698
T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C:Accession: PT0546; PT0698; PT0583
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0546

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH

A:Accession: PT0698

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE2>

A:Experimental source: newborn thymus, strain BALB/c, 135-1BP

A:Accession: PT0583

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE3>

A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 3 SG 4

RESULT 12
PT0677
T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0558; PT0677
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0558

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG

A:Accession: PT0677

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

RESULT 13
PT0706
T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

Search completed: April 21, 2003, 12:12:21
Job time : 11.6667 secs

C;Accession: PT0706
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0706
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

RESULT 14
PT0675
T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0675
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0675
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

RESULT 15
PT0566
T-cell receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0566
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0566
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
||
Db 2 SG 3

GenCore version 5.1.1.4, p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:05 ; Search time 11.3333 Seconds
(without alignments)
66.718 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFHRDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0 33473

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA.*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	9	90.0	10	9	US-09-865-294-69	Sequence 69, Appl
2	6	60.0	7	10	US-09-867-847-5	Sequence 5, Appli
3	5	50.0	4	10	US-09-972-475-36	Sequence 36, Appl
4	4	40.0	5	10	US-09-808-037-1	Sequence 1, Appli
5	4	40.0	5	10	US-09-794-927-72	Sequence 72, Appl
6	4	40.0	5	10	US-09-795-847-72	Sequence 72, Appl
7	4	40.0	5	10	US-09-794-743-72	Sequence 72, Appl
8	4	40.0	5	10	US-09-794-748-72	Sequence 72, Appl
9	4	40.0	5	10	US-09-794-925-72	Sequence 72, Appl
10	4	40.0	5	10	US-09-681-442-63	Sequence 72, Appl
11	4	40.0	6	10	US-09-808-037-7	Sequence 7, Appli
12	4	40.0	4	10	US-09-149-718-10	Sequence 10, Appl
13	4	40.0	4	10	US-09-795-903A-4	Sequence 4, Appli
14	4	40.0	10	9	US-09-795-903A-5	Sequence 5, Appli
15	4	40.0	10	10	US-09-794-927-63	Sequence 63, Appl
16	4	40.0	10	10	US-09-794-927-64	Sequence 64, Appl
17	4	40.0	10	10	US-09-795-847-63	Sequence 63, Appl
18	4	40.0	10	10	US-09-795-847-64	Sequence 64, Appl
19	4	40.0	10	10	US-09-794-743-63	Sequence 63, Appl

20	4	40.0	10	10	US-09-794-743-64	Sequence 64, Appl
21	4	40.0	10	10	US-09-794-748-63	Sequence 63, Appl
22	4	40.0	10	10	US-09-794-748-64	Sequence 64, Appl
23	4	40.0	10	10	US-09-796-264-4	Sequence 4, Appli
24	4	40.0	10	10	US-09-796-264-5	Sequence 5, Appli
25	4	40.0	10	10	US-09-794-925-63	Sequence 63, Appl
26	4	40.0	10	10	US-09-794-925-64	Sequence 64, Appl
27	4	40.0	10	10	US-09-681-442-63	Sequence 63, Appl
28	4	40.0	10	10	US-09-681-442-64	Sequence 64, Appl
29	4	40.0	10	10	US-09-845-226-4	Sequence 4, Appli
30	4	40.0	10	10	US-09-845-226-5	Sequence 5, Appli
31	3	30.0	4	9	US-10-029-191-10	Sequence 10, Appl
32	3	30.0	4	9	US-10-091-135-90	Sequence 90, Appl
33	3	30.0	4	9	US-09-848-616-88	Sequence 88, Appl
34	3	30.0	4	10	US-09-916-230-19	Sequence 19, Appl
35	3	30.0	5	8	US-08-424-550B-364	Sequence 364, App
36	3	30.0	5	9	US-09-961-721-9	Sequence 9, Appli
37	3	30.0	5	9	US-10-179-046-15	Sequence 15, Appl
38	3	30.0	5	10	US-09-910-071-18	Sequence 18, Appl
39	3	30.0	5	10	US-09-910-071-19	Sequence 19, Appl
40	3	30.0	5	10	US-09-821-831-72	Sequence 72, Appl
41	3	30.0	5	10	US-09-748-114-29	Sequence 29, Appl
42	3	30.0	6	9	US-09-727-963A-21	Sequence 21, Appl
43	3	30.0	6	9	US-10-059-749-72	Sequence 72, Appl
44	3	30.0	6	9	US-10-247-488-8	Sequence 8, Appli
45	3	30.0	6	9	US-10-091-135-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-69
; Sequence 69, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-69

Query Match 90.0%; Score 9; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEFHRDSGY 9
Db 2 AEFHRDSGY 10
|||||||

RESULT 2
US-09-867-847-5
; Sequence 5, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

;; PRIOR APPLICATION NUMBER: 60/168,594
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: 09/724,842
;; PRIOR FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
;; OTHER INFORMATION: or peptidomimetics
US-09-867-847-5

Query Match 60.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRH 6
 |||||
DB 2 AEFRRH 7

RESULT 3
US-09-972-475-36
; Sequence 36, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US98 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US98 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-972-475-36

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 HDSGY 9
 |||||
DB 1 HDSGY 5

RESULT 4
US-09-808-037-1
; Sequence 1, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-1

Query Match 40.0%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRH 5
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DB 1 EFRH 4

RESULT 5
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FC
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
 ||||
DB 2 AEFR 5

RESULT 6
US-09-795-847-72
; Sequence 72, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
 ||||
DB 2 AEFR 5

RESULT 7
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
 ||||
DB 2 AEFR 5

RESULT 8
US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPF 4
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|
|
|
Db 2 AEPF 5

RESULT 9

US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPF 4
|
|
|
|
Db 2 AEPF 5

RESULT 10
US-09-681-442-72
; Sequence 72, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPF 4
|
|
|
|
Db 2 AEPF 5

RESULT 11

US-09-808-037-7
; Sequence 7, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Elliot
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-7

Query Match 40.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRH 5
|
|
|
|
Db 3 EFRH 6

RESULT 12

US-09-149-718-10
; Sequence 10, Application US/09149718
; Patent No. US20020104104A1
; GENERAL INFORMATION:
; APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
; APPLICANT: Peter A. Seubert, and Russell E. Rydel
; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
; TITLE OF INVENTION: Therapeutics Using Transgenic Animal Models
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA

COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,487
FILING DATE:
APPLICATION NUMBER: 08/480,653
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: ANS101CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-149-718-10

Query Match 40.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
DB 2 AEFR 5

RESULT 13
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match 40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
DB 7 AEFR 10

RESULT 14
US-09-795-903A-5
; Sequence 5, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-795-903A-5

Query Match 40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
DB 7 AEFR 10

RESULT 15
US-09-794-927-63
; Sequence 63, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-63

Query Match      40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AEFR 4
       | | | |
Db      7 AEFR 10

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Job time : 11.3333 secs
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:35 ; Search time 10 Seconds
(without alignments)
29.423 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFRRHDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	90.0	10	1	US-08-371-930-12
2	9	90.0	10	5	PCT-US94-01712-12
3	5	50.0	5	4	US-08-617-267C-36
4	4	40.0	6	1	US-07-843-949A-8
5	4	40.0	6	2	US-08-218-978-8
6	4	40.0	7	3	US-08-303-861-3
7	4	40.0	7	4	US-09-173-941-82
8	4	40.0	9	6	517197-3
9	4	40.0	10	1	US-07-766-351-1
10	4	40.0	10	1	US-08-059-032-1
11	4	40.0	10	2	US-08-764-640-119
12	4	40.0	10	2	US-08-659-984A-19
13	4	40.0	10	3	US-08-973-225-119
14	4	40.0	10	3	US-09-244-298A-119
15	4	40.0	10	4	US-08-480-332-9
16	4	40.0	10	4	US-08-660-531-19
17	4	40.0	10	4	US-09-516-704-119
18	4	40.0	10	4	US-09-548-372D-63
19	4	40.0	10	4	US-09-548-372D-64
20	4	40.0	10	4	US-09-548-367D-63
21	4	40.0	10	4	US-09-548-367D-64
22	4	40.0	10	4	US-09-549-090-119
23	4	40.0	10	5	PCT-US91-07290-1
24	3	30.0	4	1	US-07-750-330-3
25	3	30.0	4	1	US-07-750-330-4
26	3	30.0	4	1	US-07-780-790A-9
27	3	30.0	4	1	US-08-022-411-5

28	3	30.0	4	2	US-08-441-871-2	Sequence 2, Appli
29	3	30.0	4	2	US-08-672-610A-33	Sequence 33, Appli
30	3	30.0	4	3	US-09-138-056-58	Sequence 58, Appli
31	3	30.0	4	4	US-09-187-859-169	Sequence 169, App
32	3	30.0	4	4	US-09-187-859-171	Sequence 171, App
33	3	30.0	4	4	US-09-513-783A-92	Sequence 92, Appli
34	3	30.0	5	1	US-07-750-330-1	Sequence 1, Appli
35	3	30.0	5	1	US-07-750-330-2	Sequence 2, Appli
36	3	30.0	5	1	US-07-750-330-5	Sequence 5, Appli
37	3	30.0	5	1	US-07-780-790A-5	Sequence 5, Appli
38	3	30.0	5	1	US-07-990-301A-9	Sequence 9, Appli
39	3	30.0	5	1	US-08-584-579-4	Sequence 4, Appli
40	3	30.0	5	1	US-08-676-263-3	Sequence 3, Appli
41	3	30.0	5	1	US-08-406-192-42	Sequence 42, Appli
42	3	30.0	5	1	US-08-749-882A-5	Sequence 5, Appli
43	3	30.0	5	1	US-08-244-415A-6	Sequence 6, Appli
44	3	30.0	5	2	US-08-545-151-42	Sequence 42, Appli
45	3	30.0	5	2	US-08-539-134-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55sx
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-12

Query Match 90.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFRRHDSGY 9
DB 2 AEFRRHDSGY 10

RESULT 2

PCT-US94-01712-12
; Sequence 12, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-01712-12

Query Match 90.0%; Score 9; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRRDSGY 9
Db 2 AEFRRDSGY 10

RESULT 3

US-08-617-267C-36
; Sequence 36, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-36

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HDSGY 9
Db 1 HDSGY 5

RESULT 4

US-07-843-949A-8
; Sequence 8, Application US/07843949A
; Patent No. 5340935
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Streuli, Michel
; TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
; TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/843,949A
; FILING DATE: 19920219
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/460,678
; FILING DATE: January 5, 1990
; APPLICATION NUMBER: 07/726,607
; FILING DATE: July 10, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/021003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-07-843-949A-8

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGYE 10
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Db 1 SGYE 4

RESULT 5
US-08-218-978-8

; Sequence 8, Application US/08218978
; Patent No. 5837811
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Streuli, Michel
; APPLICANT: Schlossman, Stuart F.
; TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
; TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,978
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/843,949
; FILING DATE: February 19, 1992
; APPLICATION NUMBER: 07/460,678
; FILING DATE: January 5, 1990
; APPLICATION NUMBER: 07/726,607
; FILING DATE: July 10, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/021003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-218-978-8

Query Match 40.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 SGYE 10
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Db 1 SGYE 4

RESULT 6

US-08-303-861-3
; Sequence 3, Application US/08303861
; Patent No. 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABLUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; TITLE OF INVENTION: VACCINES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,861
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20020.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-303-861-3

Query Match 40.0%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSGY 9
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Db 2 DSGY 5

RESULT 7

US-09-173-941-82
; Sequence 82, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NOV0081S
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-82

Query Match          40.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RHDS 7
Db 1 RHDS 4

RESULT 8
5177197-3
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 3:
; LENGTH: 9
5177197-3

Query Match          40.0%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSGY 9
Db 5 DSGY 8

RESULT 9
US-07-766-351-1
; Sequence 1, Application US/07766351
; Patent No. 5292652
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,351
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
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; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Xaa5
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-07-766-351-1

Query Match          40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFR 4
Db 7 AEFR 10

RESULT 10
US-08-059-032-1
; Sequence 1, Application US/08059032
; Patent No. 5424205
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower,
; CITY: Suite 2000
; STATE: San Francisco
; COUNTRY: California
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,032
; FILING DATE: 19930507
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William E.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= Xaa4
OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
FEATURE:
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LOCATION: 5
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OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-08-059-032-1

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
Db 7 AEFR 10

RESULT 11
US-08-764-640-119
Sequence 119, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprence, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-119
Query Match 40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEFR 4
Db 4 AEFR 7
RESULT 12
US-08-659-984A-19
Sequence 19, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-0028100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: one-of(1)
OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
US-08-659-984A-19
Query Match 40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEFR 4
Db 7 AEFR 10

RESULT 13

US-08-973-225-119
; Sequence 119, Application US/08973225A
; Patent No. 6083313
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:

US-08-973-225-119

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

RESULT 14

US-09-244-298A-119
; Sequence 119, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprince, Randolph B.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:

US-08-973-225-119

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

RESULT 15

US-08-480-332-9
; Sequence 9, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; Applicant: Barenholz, Yecheskel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/316,436

US-08-480-332-9

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-119

US-09-244-298A-119

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

RESULT 15

US-08-480-332-9
; Sequence 9, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; Applicant: Barenholz, Yecheskel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/316,436

US-08-480-332-9

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

RESULT 15

US-08-480-332-9
; Sequence 9, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; Applicant: Barenholz, Yecheskel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/316,436

US-08-480-332-9

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEF 4
Db 4 AEF 7

RESULT 15

US-08-480-332-9
; Sequence 9, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; Applicant: Barenholz, Yecheskel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/316,436

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; FILING DATE: 29-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/035,443
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOHR, JUDY M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5325-0115.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Peptide 9, Fig. 13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-480-332-9

Query Match 40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 DSGY 9
   ||||
Db 3 DSGY 6

Search completed: April 21, 2003, 12:12:57
Job time : 11 secs
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:03:55 ; Search time 28 Seconds
(without alignments)
309.071 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSNGKAIIGLMVGGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	217	100.0	82	Q16019	Q16019 homo sapien
3	217	100.0	82	Q16020	Q16020 homo sapien
4	217	100.0	82	P78438	P78438 homo sapien
5	217	100.0	534	13 Q93296	Q93296 gallus gall
6	217	100.0	569	13 Q9PVL1	Q9PVL1 gallus gall
7	217	100.0	695	11 Q95KN7	Q95KN7 macaca fasc
8	217	100.0	695	11 Q60496	Q60496 cavia sp. p
9	217	100.0	695	13 Q9DGJ8	Q9DGJ8 gallus gall
10	217	100.0	751	13 Q9DGJ7	Q9DGJ7 gallus gall
11	217	100.0	770	6 Q8TUI0	Q8TUI0 sus scrofa
12	207	95.4	97	4 Q13778	Q13778 homo sapien
13	198	91.2	79	11 Q35463	Q35463 cricetus
14	198	91.2	607	11 Q99K32	Q99K32 mus musculus
15	198	91.2	693	13 Q98SG0	Q98SG0 xenopus lae
16	198	91.2	695	11 P97487	P97487 mus musculus

17	198	91.2	747	13	Q91963	Q91963 xenopus. ap
18	195	89.9	695	13	Q98SF9	Q98SF9 xenopus lae
19	188	86.6	699	13	O57394	O57394 narke japon
20	176	81.1	33	4	Q9UC33	Q9UC33 homo sapien
21	175	80.6	780	13	O73683	O73683 tetraodon f
22	171	78.8	737	13	O93279	O93279 fuju rubrip
23	162	74.7	30	4	Q9UCA9	Q9UCA9 homo sapien
24	157.5	72.6	357	13	O8UUI8	O8UUI8 brachydanio
25	157.5	72.6	472	13	Q8UUS0	Q8UUS0 brachydanio
26	157.5	72.6	612	13	Q919E7	Q919E7 brachydanio
27	157.5	72.6	738	13	Q90W28	Q90W28 brachydanio
28	156	71.9	239	13	O8UUI7	O8UUI7 brachydanio
29	156	71.9	694	13	O8UUR9	O8UUR9 brachydanio
30	147	67.7	28	4	Q9UCD1	Q9UCD1 homo sapien
31	121	55.8	49	6	O97917	O97917 bos taurus
32	106	48.8	19	4	O9UCC8	O9UCC8 homo sapien
33	95	43.8	35	4	O8WZ99	O8WZ99 homo sapien
34	64	29.5	328	2	O9RPS4	O9RPS4 enterococcu
35	63	29.0	321	16	O8RG41	O8RG41 fusobacteri
36	63	29.0	755	2	O9R717	O9R717 agrobacteri
37	63	29.0	755	2	O9R472	O9R472 agrobacteri
38	63	29.0	755	2	O9R694	O9R694 agrobacteri
39	63	29.0	755	16	Q8U6A3	Q8U6A3 agrobacteri
40	62	28.6	755	2	Q44388	Q44388 agrobacteri
41	60	27.6	755	2	O9WWA1	O9WWA1 agrobacteri
42	59	27.2	20	4	O9UCB6	O9UCB6 homo sapien
43	57.5	26.5	895	10	Q9AWB6	Q9AWB6 lycopersico
44	57	26.3	195	10	O22662	O22662 arabidopsis
45	57	26.3	332	12	Q9DQNS	Q9DQNS potato viru

ALIGNMENTS

RESULT 1

Q16014 ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -;
DR HSSP; P05067; IBA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 217; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNGKATIGLMVGGVVIA 42

|||||
Db 18 DAEFRHDSGYEVHHQKLVFFAEDVGSNGKATIGLMVGGVVIA 59

RESULT 2

Q16019 ID Q16019 PRELIMINARY; PRT; 82 AA.

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AC Q16019;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 217; DB 4; Length 82;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 59

RESULT 3
Q16020
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26265.2; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5A5D9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 217; DB 4; Length 82;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 59

RESULT 4
P78438

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ID P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (Beta-amyloid protein). (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RT Little S.P.;
RA "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RL linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'Dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RL kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -
DR EMBL; S45136; AAB23646.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 217; DB 4; Length 82;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 58

RESULT 5
O93296
ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a

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RT substrate for caspase-3 in dying motoneurons. ";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 217; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 477

RESULT 6

Q9PVL1 PRELIMINARY; PRT; 569 AA.
ID Q9PVL1
AC Q9PVL1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;

RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -;
DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 217; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 472 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 513

RESULT 7

Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7

AC Q95KN7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Amyloid b-protein precursor.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlinsky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -;
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT SIGNAL 17
FT CHAIN 597 636
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 217; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 638

RESULT 8

Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496

AC Q60496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE putative amyloid precursor protein.

OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CAA66230.1; -;
DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 217; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

Db 597 DAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIA 638

RESULT 9

O9DGJ8 PRELIMINARY; PRT; 695 AA.

AC O9DGJ8; 1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 217; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIA 42

Db 597 DAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIA 638

RESULT 10

O9DGJ7 PRELIMINARY; PRT; 751 AA.

AC O9DGJ7; 1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD00022; Kunitz_BPTI; 1.

Query Match 100.0%; Score 217; DB 6; Length 770;

Best Local Similarity 100.0%; Pred. No. 2.7e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIA 42

Db 672 DAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIA 713

RESULT 12

O13778 PRELIMINARY; PRT; 97 AA.

AC O13778; 1
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (AD-AP) (Fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldhaber D., Lerman M.I., McBride O.W., Saffioti U., Cajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 brain amyloid of Alzheimer's disease.";
 RL Science 235:877-880(1987).
 DR EMBL; M15533; AAA35540.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR NON_TER 1
 FT SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;
 SQ
 Query Match 95.4%; Score 207; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.5e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 Db 1 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 40
 RESULT 13
 Q35463
 ID O35463 PRELIMINARY; PRT; 79 AA.
 AC O35463;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN BETA APP.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR NON_TER 1
 FT NON_TER 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BF3F597 CRC64;
 Query Match 91.2%; Score 198; DB 11; Length 79;
 Best Local Similarity 92.9%; Pred. No. 7.6e-20;
 Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 Db 21 DAEFGHDSGFEVRRHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 62
 RESULT 14
 Q99K32
 ID Q99K32 PRELIMINARY; PRT; 607 AA.
 AC Q99K32;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 68.4 kDa protein (Fragment).
 GN APP.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005490; AAH05490.1; -.
 DR HSSP; P05067; IAAAP.
 DR MGD; MGI:88059; App.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Hypothetical protein; Serine protease inhibitor.
 FT NON_TER 1
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;
 Query Match 91.2%; Score 198; DB 11; Length 607;
 Best Local Similarity 92.9%; Pred. No. 8.8e-19;
 Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 Db 509 DAEFRHDSGFEVRRHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 550
 RESULT 15
 Q98SG0
 ID Q98SG0 PRELIMINARY; PRT; 693 AA.
 AC Q98SG0;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-amyloid precursor protein A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -.
 DR HSSP; P05067; IHZ3.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW SIGNAL.
 FT SIGNAL
 SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655CIAB653 CRC64;
 Query Match 91.2%; Score 198; DB 13; Length 693;
 Best Local Similarity 88.1%; Pred. No. 1e-18;
 Matches 37; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:01:04 ; Search time 11 seconds
(without alignments)
158.364 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHQKLVFF.....DVGSNKGAIILMGVGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	57	A4_PIG	Q29023 sus scrofa
2	217	100.0	57	A4_URSMA	Q29149 ursus marit
3	217	100.0	58	A4_CANFA	Q28280 canis famil
4	217	100.0	58	A4_RABIT	Q28748 oryctolagus
5	217	100.0	58	A4_SHEEP	Q28757 ovis aries
6	217	100.0	59	A4_BOVIN	Q28053 bos taurus
7	217	100.0	751	A4_SAISC	Q35241 salmuri scl
8	217	100.0	770	A4_HUMAN	P05067 homo sapien
9	198	91.2	770	A4_MOUSE	P12023 mus musculu
10	198	91.2	770	A4_RAT	P08592 rattus norv
11	62	28.6	755	TR2M_AGRV4	P04029 agrobacteri
12	61	28.1	755	TR2N_AGRV1	P25017 agrobacteri
13	57	26.3	327	POLG_PVYCH	P21234 potato viru
14	57	26.3	503	Y226_MYCPN	P75462 mycoplasma
15	56.5	26.0	378	SLG1_YEAST	P54867 saccharomyc
16	55.5	25.6	297	FTR_ARCFU	O28076 archaeoglob
17	55	25.3	488	DHAL_PSESP	P33008 pseudomonas
18	55	25.3	3063	POLG_PVYN	P18247 p genome po
19	54.5	25.1	967	PDB1_ARATH	P33733 arabidopsis
20	54	24.9	284	POLG_PVYVO	P11897 potato viru
21	53.5	24.7	708	YNZB_CAEEL	P45972 caenorhabdi
22	53.5	24.0	971	Y228_BORBU	O51246 borrelia bu
23	52	24.0	611	YCR3_YEAST	P25351 saccharomyc
24	51	23.5	494	COBQ_MYCTU	O53677 mycobacteri
25	51	23.5	769	ITB2_BOVIN	P32592 bos taurus
26	50.5	23.3	915	PDB2_ARATH	O23078 arabidopsis
27	50	23.0	285	MENB_HAEIN	P44960 haemophilus
28	50	23.0	1437	MRP5_HUMAN	O15440 homo sapien
29	50	23.0	3579	STAN_DROME	Q9V5N8 drosophila
30	49.5	22.8	1162	VGL2_IBVM	P12651 avian infec
31	49	22.6	246	TPIS_CULTA	P30741 culcx tarsa
32	49	22.6	322	Y853_RICPR	Q9ZCA7 rickettsia
33	49	22.6	403	PGK_STRCO	Q9Z519 streptomyce

34	49	22.6	432	1	PURA_RHILLO	Q98F97 rhizobium l
35	49	22.6	568	1	NIRS_PSEAE	P24474 pseudomonas
36	49	22.6	674	1	TMLI_ARATH	P33543 arabidopsis
37	49	22.6	704	1	SSP2_BOMMO	P20613 bombyx mori
38	49	22.6	753	1	PPE2_HUMAN	O14830 homo sapien
39	49	22.6	757	1	PPE2_MOUSE	O35385 mus musculu
40	49	22.6	1080	1	HDC_DROME	Q9N2M8 drosophila
41	48.5	22.4	160	1	FMDR_ECOLI	P24093 escherichia
42	48.5	22.4	330	1	COAT_PEMV	P07993 pepper mott
43	48.5	22.4	393	1	GUNI_USTMA	P54424 ustilago ma
44	48.5	22.4	459	1	Y226_MYCGE	P47468 mycoplasma
45	48.5	22.4	497	1	GLYA_CHLPN	Q9Z831 chlamydia p

ALIGNMENTS

RESULT 1
A4_PIG STANDARD; PRT; 57 AA.
AC Q29023; 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN App.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=165167;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56127; CAA39592.1; -
CC HSSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 |||
 DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 2

ID A4_URSUMA STANDARD; PRT; 57 AA.
 AC Q23149;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 OX NCBI_TaxID=29073;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC
 CC EMBL; X56128; CAA39593.1; -
 CC HSSP; P05067; 1BA4.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR001255; Beta-APP.
 CC Pfam: PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC NON_TER 1 1
 CC CHAIN 1 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 34 57
 CC NON_TER 57 57
 CC SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 7.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 |||
 DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 3

ID A4_CANFA STANDARD; PRT; 58 AA.
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC
 CC EMBL; X56125; CAA39590.1; -
 CC HSSP; P05067; 1BA4.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR001255; Beta-APP.
 CC Pfam: PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC NON_TER 1 1
 CC CHAIN 1 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 35 58
 CC NON_TER 58 58
 CC SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 |||
 DB 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 48

RESULT 4

ID A4_RABIT STANDARD; PRT; 58 AA.
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 DR EMBL; X56129; CAA39594.1; -;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 SQ
 Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 47
 RESULT 5
 A4_SHEEP
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA MEDLINE=92017079; PubMed=1656157;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----

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 CC -----
 DR EMBL; X56130; CAA39595.1; -;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 SQ
 Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 47
 RESULT 6
 A4_BOVIN
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=92017079; PubMed=1656157;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 DR EMBL; X56124; CAA39589.1; -;
 DR EMBL; X56126; CAA39591.1; -;

DR	Pfam:	PF03494;	Beta-APP; 1.
DR	PRINTS:	PR00203;	AMYLOIDA4.
DR	PRINTS:	PR00759;	BASICPTASE.
DR	PfDom:	PD000222;	Kunitz_BPTI; 1.
DR	SMART:	SM00006;	A4_EXTRA; 1.
DR	SMART:	SM00131;	KU; 1.
DR	PROSITE:	PS00319;	A4_EXTRA; 1.
DR	PROSITE:	PS00320;	A4_INTRA; 1.
DR	PROSITE:	PS00280;	BPTI_KUNITZ_1; 1.
DR	PROSITE:	PS0279;	BPTI_KUNITZ_2; 1.
KW	Glycoprotein:	Amyloid;	Neurone; Transmembrane; Alternative splicing;
KW	Signal;	Serine protease inhibitor.	
FT	SIGNAL	1	17
FT	CHAIN	18	751
FT	CHAIN	653	695
FT	DOMAIN	18	680
FT	TRANSMEM	681	704
FT	DOMAIN	705	751
FT	DOMAIN	287	345
FT	SITE	740	743
FT	ACT_SITE	301	302
FT	DISULFID	291	341
FT	DISULFID	300	324
FT	DISULFID	316	337
FT	CARBOHYD	523	523
FT	CARBOHYD	552	552
FT	SEQUENCE	751 AA;	84893 MW; 6C3E431089569049 CRC64;
QY	Query Match	100.08;	Score 217; DB 1; Length 751;
QY	Best Local Similarity	100.08;	Pred. No. 1.le-20;
Matches	42;	Conservative	0; Mismatches 0; Indels 0; Gaps
DQ	1	DAEFRHDSGYEHVHQKLVFFAEDVGSNKGAIIGLMVGGVIA	42
DQ	1		
DB	653	DAEFRHDSGYEHVHQKLVFFAEDVGSNKGAIIGLMVGGVIA	694
RESULT 8			
A4_HUMAN			
ID	A4_HUMAN	STANDARD;	PRT; 770 AA.
AC	P05067;	P09000;	Q16011;
DT	13-AUG-1987	(Rel. 05,	Created)
DT	01-NOV-1991	(Rel. 20,	Last sequence update)
DT	16-OCT-2001	(Rel. 40,	Last annotation update)
DE	Alzheimer's disease amyloid A4 protein precursor	(Protease nexin-II-I)	
DE	(PN-II) (APPI) [Contains: Beta-amyloid protein	(Beta-App) (A-beta)]	
GN	APP OR A4 OR CVAP OR AD1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=871444572;	PubMed=2881207;	
RX	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,		
RX	Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;		
RT	"The precursor of Alzheimer's disease amyloid A4 protein resembles		
RT	cell-surface receptor."		
RL	Nature 325:733-736(1987).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88122639;	PubMed=2893289;	
RA	Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,		
RA	Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,		
RA	Cordell B.;		
RT	"A new A4 amyloid mRNA contains a domain homologous to serine		
RT	proteinase inhibitors."		
RL	Nature 331:525-527(1988).		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89128427;	PubMed=2783775;	
RX	Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,		

RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RL is encoded by 16 exons";
 RN Nucleic Acids Res. 17:517-522(1989).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RT Saito M., Tsukuni S., Sakaki Y.;
 RA "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus";
 RN Nucleic Acids Res. 25:1802-1808(1997).
 [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RT Gusella J.F., Neve R.L.;
 RA "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease";
 RN Nature 331:528-530(1988).
 [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity";
 RN Nature 331:530-532(1988).
 [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RT Marotta C.A.;
 RA "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex";
 RN Proc. Natl. Acad. Sci. U.S.A. 85:928-933(1988).
 [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RT Tourtellotte W.W., Huebner V., Shively J.E.;
 RA "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels";
 RN J. Neurochem. 49:1394-1401(1987).
 [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene";
 RN Gene 87:257-263(1990).
 [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide";
 RN Nucleic Acids Res. 16:9351-9351(1988).
 [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts";
 RN J. Biol. Chem. 262:8508-8514(1987).

RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II";
 RN Nature 341:144-147(1989).
 [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor";
 RN Biochem. Biophys. Res. Commun. 167:716-721(1990).
 [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)";
 RN Nature 362:75-79(1993).
 [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein";
 RN Nat. Struct. Biol. 6:327-331(1999).
 [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor";
 RN Biochemistry 29:10018-10022(1990).
 [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,
 RA Kamareck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein";
 RN Biochemistry 30:10467-10478(1991).
 [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafoos J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide";
 RN Biochemistry 33:7788-7796(1994).
 [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment";
 RN Biochemistry 35:16094-16104(1996).
 [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RN Biochemistry 37:11064-11077(1998).
 [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;

RA Poulson S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RN STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Meggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 QY Query Match 100.0%; Score 217; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.le-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAERFHDGSEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42
 DB 672 DAERFHDGSEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 713
 RESULT 9
 AA_MOUSE
 ID A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A..
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A..
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sakaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RN Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A..
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]

RP SEQUENCE OF 1-19 FROM N.A..
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sakaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 DR EMBL; X59379; ; NOT ANNOTATED_CDS.
 DR EMBL; M18373; AAA37139.1; .
 DR EMBL; X15210; CAA33280.1; .
 DR EMBL; D10603; BAA01456.1; .
 DR EMBL; M24397; BAA39929.1; .
 DR PIR; A27485; A27485.
 DR PIR; S04855; S04855.
 DR PIR; S19727; S19727.
 DR HSP; P05067; LAAP.
 DR MGD; MGI:88059; App.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PRINTS; PRO0759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT TRANSMEM
 FT DOMAIN 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT EQUIVALENT OF BETA-AMYLOID PROTEIN.

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FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR
FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
FT VARSPLIC 346 380 MISSING (IN ISOFORM APP(751)).
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

Query Match
Best Local Similarity 91.2%; Score 198; DB 1; Length 770;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGWVIA 42
DB 672 DAEFGHDSGFVHRHOKLVFAEDVGSNGKAIIGLMVGWVIA 713

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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or send an email to license@isb-sib.ch).
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DR EMBL; X07648; CAA30488.1; -;
DR EMBL; X14066; CAA32229.1; -;

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DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770 BY SIMILARITY.
FT FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT FT HOMOLOG.
FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723 POTENTIAL.
FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D68B2D929A7 CRC64;

Query Match
Best Local Similarity 91.2%; Score 198; DB 1; Length 770;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGWVIA 42
DB 672 DAEFGHDSGFVHRHOKLVFAEDVGSNGKAIIGLMVGWVIA 713

RESULT 11
TR2M_AGR4
ID TR2M_AGR4 STANDARD; PRT; 755 AA.
AC P04029;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN TMS1.
OS Agrobacterium tumefaciens (strain Ach5), and
OS Agrobacterium tumefaciens.
OG Plasmid pTiAch5, and Plasmid pTiAGNC.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176298, 358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ach5; PLASMID=pTiAch5;
RX MEDLINE=84207942; PubMed=6327292;
RA Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
RA Lemmers M., van Montagu M., Schell J.;
RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium
RT tumefaciens plasmid pTiAch5.";
RL EMBO J. 3:835-846(1984).
RN [2]
RP SEQUENCE FROM N.A.

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RC PLASMID=PTIA6NC;
RX MEDLINE=84170374; PubMed=6584906;
RA Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
RA Fuller S., Flores C., Peschon J., Nester E., Gordon M.;
RT "Nucleotide sequence of the tms genes of the PTIA6NC octopine T1
RT plasmid: two gene products involved in plant tumorigenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.
CC -1- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02554; AAA92550.1; -.
CC PIR; A04497; QQAG4T.
CC InterPro; IPR002937; Amino_oxidase.
CC InterPro; IPR000624; Glycosidase.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF01593; Amino_oxidase; 1.
CC Pfam; PF02027; RolB_RolC; 1.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
CC T-DNA; Plasmid.
CC VARIANT 718 719 NR -> IQ (IN PTIA6NC).
CC VARIANT 721 721 P -> A (IN PTIA6NC).
CC SEQUENCE 755 AA; 83947 MW; 9FD2B83FEA001A4D CRC64;
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CC Query Match 28.6%; Score 62; DB 1; Length 755;
CC Best Local Similarity 41.7%; Pred. No. 1.9;
CC Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;
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CC QY 7 DSGYEVHVKLVFAEDVGSNGKAIIGLMVGGVVIA 42
CC ||| ::||| ||| |::| |::| |::|
CC 223 DSG-----RIGFFPEDVPRKPVAVIGAGISGLVVA 252
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CC RESULT 12
CC TR2N_AGRVI STANDARD; PRT; 755 AA.
CC AC P25017;
CC DT 01-MAR-1992 (Rel. 21, Created)
CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
CC GN IAAH.
CC OS Agrobacterium vitis (Rhizobium vitis).
CC OG Plasmid pT1M4.
CC OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC OC Rhizobiaceae; Rhizobium.
CC OX NCBI_TaxID=373;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=TM4;
CC RX MEDLINE=91329707; PubMed=1868204;
CC RA Bonnard G., Vincent F., Otten L.;
CC RT "Sequence of Agrobacterium tumefaciens biotype III auxin genes.";
CC RL plant Mol. Biol. 16:733-738(1991).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=CG474;
CC RA Otten L., de Ruffray P.;
CC RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.

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CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
CC -1- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC -1- SIMILARITY: STRONG, WITH ITS COUNTERPARTS FROM A. TUMEFACIENS
CC PLASMIDS PT15955, PTACH5 AND PTIAGNC.
CC -1- CAUTION: THE PLASMID PT1M4 CARRIES TWO T-REGIONS, THE TA AND
CC TB REGION, BOTH OF WHICH HAVE A FUNCTIONAL IAAH GENE, WITH LOW
CC HOMOLOGY BETWEEN THEM.
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CC -----
CC EMBL; X56185; CAA39646.1; -.
CC EMBL; U83987; AAB41874.1; -.
CC PIR; S15450; DAAGWT.
CC PIR; S15002; S15002.
CC InterPro; IPR002937; Amino_oxidase.
CC InterPro; IPR000624; Glycosidase.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF01593; Amino_oxidase; 1.
CC Pfam; PF02027; RolB_RolC; 1.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
CC T-DNA; Plasmid.
CC SEQUENCE 755 AA; 83972 MW; 6FA63E502343136F CRC64;
CC
CC Query Match 28.1%; Score 61; DB 1; Length 755;
CC Best Local Similarity 41.7%; Pred. No. 2.6;
CC Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;
CC
CC QY 7 DSGYEVHVKLVFAEDVGSNGKAIIGLMVGGVVIA 42
CC ||| ::||| ||| |::| |::| |::|
CC 223 DSG-----RIGFFPEDVPRKPVAVIGAGISGLVVA 252
CC
CC RESULT 13
CC POLG_PVYCH STANDARD; PRT; 327 AA.
CC AC P21294;
CC DT 01-MAY-1991 (Rel. 18, Created)
CC DT 01-MAY-1991 (Rel. 18, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Genome polyprotein [Contains: Nuclear inclusion protein B (NI-B) (NIB)
CC (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)]
CC (Fragment).
CC OS Potato virus Y (strain Chinese isolate) (PVY).
CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
CC OC Potyvirus.
CC OX NCBI_TaxID=12218;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91016851; PubMed=2216735;
CC RA Zhou X.R., Fang R.X., Wang K.Q.;
CC RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese
CC isolate).";
CC RL Nucleic Acids Res. 18:5554-5554(1990).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
CC -----
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DR EMBL: X54058; CRA37993.1; -;
DR PIR: S11549; S11549.
DR InterPro: IPR001592; Poty_coat.
DR Pfam: PF00767; Poty_coat; 1.
KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
FT NON_TER 1
FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 61 327 COAT PROTEIN.
SQ SEQUENCE 327 AA; 36968 MW; 8F8355E2DE6F2F18 CRC64;

Query Match 26.3%; Score 57; DB 1; Length 327;
Best Local Similarity 53.1%; Pred. No. 3.7;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEPFRHDSGYEVHHQKLVFFAED-----VGSNKH 28
DB 47 DDEFEFDS-YEVHHQ-----ANDTIDAVGDNK 72

RESULT 14

Y226_MYCPN STANDARD; PRT; 503 AA.
AC P75462;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG226 homolog (F10_orf503).
GN MPN319 OR MP517.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: TO M.GENTILIUM MG225.

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CC or send an email to license@isb-sib.ch).

CC EMBL: AE000051; AB996165.1; -;
DR InterPro: IPR002293; AA/re1_primease1.
DR InterPro: IPR004841; Permease.
DR Pfam: PF00324; aa_permeases; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 215 235 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 359 379 POTENTIAL.
FT TRANSMEM 405 425 POTENTIAL.
FT TRANSMEM 443 463 POTENTIAL.
FT TRANSMEM 468 488 POTENTIAL.
SQ SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match 26.3%; Score 57; DB 1; Length 503;
Best Local Similarity 61.1%; Pred. No. 5.7;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 24 VGSNKGAIIGLMVGGVVI 41
DB 131 VKDNGALIGLLVGGFVL 148

RESULT 15

SLGL_YEAST STANDARD; PRT; 378 AA.
AC P54867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SLG1 protein precursor.
GN SLG1 OR YOR008C OR UNF378.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bettignies G., Bergez-Aullo P., Barthe C., Louvet O.,
RA Peypouquet M.F., Morel C., Doignon F., Crouzet M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051599; PubMed=8896276;
RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
RT which correspond to previously identified genes.";
RL Yeast 12:1091-1095(1996).
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CC EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAA99196.1; -;
DR SGD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 378 SLG1 PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 378 AA; 39270 MW; EEEL64F2374CCCE3 CRC64;

Query Match 26.0%; Score 56.5; DB 1; Length 378;
Best Local Similarity 42.4%; Pred. No. 5;
Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

QY 8 SGVEVHHQKLVFFAEDVGSNKGAIIGLMVGGV 40
DB 251 SGSKTHKKK-----ANVGAIVGGVGGV 274

Search completed: April 21, 2003, 12:06:47
Job time : 14 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:05:20 ; Search time 18 seconds
(without alignments)
224.314 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSNGKAIIGLMVGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	217	100.0	42	2 PN0512	beta-amyloid prote
2	217	100.0	57	2 E60045	Alzheimer's diseas
3	217	100.0	57	2 F60045	Alzheimer's diseas
4	217	100.0	57	2 G60045	Alzheimer's diseas
5	217	100.0	57	2 D60045	Alzheimer's diseas
6	217	100.0	57	2 B60045	Alzheimer's diseas
7	217	100.0	57	2 B60045	Alzheimer's diseas
8	217	100.0	82	2 PQ0438	Alzheimer's diseas
9	217	100.0	695	1 A49795	Alzheimer's diseas
10	217	100.0	770	1 QRHUA4	Alzheimer's diseas
11	198	91.2	695	2 A27485	Alzheimer's diseas
12	198	91.2	695	2 S00550	Alzheimer's diseas
13	198	91.2	747	2 JH0773	Alzheimer's diseas
14	133	61.3	33	2 S23094	beta-amyloid prote
15	63	29.0	755	2 A13228	tryptophan 2-monoo
16	62	28.6	755	1 QOAG4T	tryptophan 2-monoo
17	61	28.1	755	1 DAAGWT	genome polyprotein
18	57	26.3	327	2 S11435	general amino acid
19	57	26.3	503	2 S73843	SLGI protein - yea
20	56.5	26.0	378	2 S61992	formylmethanofuran
21	55.5	25.6	297	2 G69525	3-methyl-2-oxobuta
22	55.5	25.6	678	2 G71526	glycosyl transfera
23	55	25.3	291	2 F95015	glycosyl transfera
24	55	25.3	317	2 H97888	probable aldehyde
25	55	25.3	488	2 S27652	genome polyprotein
26	55	25.3	3063	2 JS0166	3-methyl-2-oxobuta
27	54.5	25.1	678	2 C81683	phospholipase D [i
28	54.5	25.1	832	2 H84848	feoA-like protein,
29	54	24.9	77	2 C97027	

30	54	24.9	284	2	S04723	genome polyprotein
31	54	24.9	763	2	AI3443	Na+/H+ antiporter
32	53.5	24.7	708	2	T24727	hypothetical prote
33	53.5	24.7	971	2	D70128	conserved hypothet
34	53	24.4	256	2	G96774	hypothetical prote
35	53	24.4	390	2	C75103	na+/h+ antiporter
36	53	24.4	422	2	D72302	hypothetical prote
37	53	24.4	601	2	T02581	nodulin-like prote
38	53	24.4	1555	2	JT0959	polyprotein - pota
39	52.5	24.2	314	2	F86805	cation transporter
40	52.5	24.2	678	2	C86495	hypothetical prote
41	52.5	24.2	678	2	H72128	3-methyl-2-oxobuta
42	52	24.0	272	2	F70979	hypothetical prote
43	52	24.0	339	2	A81351	signal transductio
44	52	24.0	417	2	F70132	conserved hypothet
45	52	24.0	527	2	TI8232	conserved hypothet

ALIGNMENTS

RESULT 1

PN0512

beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653; PMID:7685598

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 217; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 7.5e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFFAEDVGSNGKAIIGLMVGVVIA 42

|||||

Db 1 DAEFRHDSGYEVHHQKLVFFFAEDVGSNGKAIIGLMVGVVIA 42

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFFAEDVGSNGKAIIGLMVGVVIA 42

|||||

Db 6 DAEFRHDSGYEVHHQKLVFFFAEDVGSNGKAIIGLMVGVVIA 47

RESULT 3

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA9592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
|||||

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
|||||

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
|||||

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
|||||

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
|||||

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; G60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 217; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLMVGGVWIA 42
|||||
DB 17 DAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLMVGGVWIA 58
|||||

RESULT 9

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a F
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing

Query Match 100.0%; Score 217; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLMVGGVWIA 42
|||||
DB 597 DAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLMVGGVWIA 638
|||||

RESULT 10

QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-p
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
A:Reference number: A33260; MUID:89392030; PMID:2675937
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:gl78863; PIDN:AAA51768.1; PID:gl78865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <VOS1>
A:Cross-references: GB:M33112; NID:gl78613; PIDN:AA859502.1; PID:gl78616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPIVPAFWKAVGR' <VOS2>
A:Cross-references: GB:M34875; NID:gl78608; PIDN:AA859501.1; PID:gl78615
R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemc
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:gl78618; PIDN:AAA51727.1; PID:gl78620
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:AA819991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AA823645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA

A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Kamakishina, N.; Wolfe, G.; Wisniewski, H.M.; Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.; Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYZ>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g292612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Experimental source: form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.; Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibit
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>

A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g9292611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, Query Match 100.0%; Score 217; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 42
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DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 713
RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.; Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:de Strooper, B.; van Leeuwen, F.; van den Berghe, H.; Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y. Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>

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[illegible]

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Search completed: April 21, 2003, 12:07:46
Job time : 20 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:06:50 ; Search time 15 Seconds
(without alignments)
211.719 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAERFHDGSEVHHQKLVFF.....DVGSNKGAIIGLMVGGVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	217	100.0	42	8	US-08-923-055-2
2	217	100.0	42	9	US-10-051-496-2
3	217	100.0	42	9	US-10-082-804-7
4	217	100.0	42	9	US-09-962-955C-37
5	217	100.0	42	9	US-09-848-616-174
6	217	100.0	42	9	US-09-865-294-65
7	217	100.0	42	10	US-09-867-847-1
8	217	100.0	42	10	US-09-956-625-26
9	217	100.0	42	10	US-09-731-460-1
10	217	100.0	43	9	US-10-076-708-7
11	217	100.0	43	9	US-10-051-496-1
12	217	100.0	43	9	US-10-217-459-1
13	217	100.0	43	10	US-09-280-966-1
14	217	100.0	43	10	US-09-904-987-1
15	217	100.0	43	10	US-09-808-037-3
16	217	100.0	43	10	US-09-866-712-3
17	217	100.0	43	10	US-09-972-475-1
18	217	100.0	43	10	US-09-992-800-1
19	217	100.0	43	10	US-09-895-443-1

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21	217	100.0	43	10	US-09-992-994-1	Sequence 1, Appli
22	217	100.0	43	10	US-09-984-834-1	Sequence 1, Appli
23	217	100.0	43	12	US-10-041-605-1	Sequence 1, Appli
24	217	100.0	53	10	US-09-797-543-5	Sequence 5, Appli
25	217	100.0	53	12	US-10-016-717-1	Sequence 1, Appli
26	217	100.0	70	10	US-09-153-076-14	Sequence 14, Appli
27	217	100.0	82	9	US-09-848-616-173	Sequence 173, App
28	217	100.0	99	9	US-10-183-119-2	Sequence 2, Appli
29	217	100.0	100	10	US-09-794-975-4	Sequence 4, Appli
30	217	100.0	103	10	US-09-972-475-2	Sequence 2, Appli
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32	217	100.0	117	9	US-09-422-569-10	Sequence 10, Appli
33	217	100.0	117	10	US-09-794-975-6	Sequence 6, Appli
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37	217	100.0	695	10	US-09-794-927-12	Sequence 12, Appli
38	217	100.0	695	10	US-09-794-927-14	Sequence 14, Appli
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45	217	100.0	695	10	US-09-794-748-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-923-055-2
; Sequence 2, Application US/08923055
; Patent No. US20010016327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: & No. US20010016327A1ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,055
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori V. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-923-055-2

Query Match 100.0%; Score 217; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEVDGSGNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHOKLVFFAEVDGSGNKGAIIGLMVGGVVIA 42

RESULT 2

US-10-051-496-2
Sequence 2, Application US/10051496
Publication No. US20020182660A1

GENERAL INFORMATION:

APPLICANT: Kei-Lai L. Fong
TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39) and Abeta(1-41), Abeta(1-42) and Abeta(1-43)

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kei-Lai L. Fong
STREET: 1004 West 8th Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US20020182660A1epad

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,496

FILING DATE: 18-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/784,854A

FILING DATE: 16-Feb-2001

APPLICATION NUMBER: 60/183,407

FILING DATE: 18-February-2000

ATTORNEY/AGENT INFORMATION:

NAME: Koenig, C. Frederick III

REGISTRATION NUMBER: 29,662

REFERENCE/DOCKET NUMBER: PBI-PT001.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-6400

TELEFAX: (215) 568-6499

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 Amino Acid

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: Protein

FEATURE:

NAME/KEY: Signal Sequence

LOCATION: 1-42

IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-051-496-2

Query Match

100.0%; Score 217; DB 9; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAEFRHDSGYEVHHOKLVFFAEVDGSGNKGAIIGLMVGGVVIA 42

RESULT 3

US-10-082-804-7

Sequence 7, Application US/10082804

Publication No. US20020194632A1

GENERAL INFORMATION:

APPLICANT: McConlogue, Lisa

APPLICANT: Gurney, Mark E.

TITLE OF INVENTION: Transgenic Knockouts of BACE-1

FILE REFERENCE: MBH 02-329-A

CURRENT APPLICATION NUMBER: US/10/082,804

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/271,092

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/271,514

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/293,762

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 42

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: A-beta 42 sequence.

US-10-082-804-7

Query Match

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Best Local Similarity 100.0%; Pred. No. 1.5e-22;

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DB 1 DAEFRHDSGYEVHHOKLVFFAEVDGSGNKGAIIGLMVGGVVIA 42

RESULT 4

US-09-962-955C-37

Sequence 37, Application US/09962955C

Publication No. US20030013648A1

GENERAL INFORMATION:

APPLICANT: Gerardo M. Castillo

APPLICANT: Alan D. Snow

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrick M. Dwyer

STREET: ProteoTech, Inc, 1818 Westlake Avenue N, Suite 114

CITY: Seattle

STATE: WA (Washington)

COUNTRY: United States of America

ZIP: 98109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC

OPERATING SYSTEM: Windows 98

SOFTWARE: WordPerfect 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,955C

FILING DATE: 24-September-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/938,275

FILING DATE: 22-August-2001

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:


```
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTEO.P03CI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: Also referred to in the specification as "AB 1-42"
US-09-962-955C-37

Query Match          100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 5
US-09-848-616-174
; Sequence 174, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
US-09-848-616-174

Query Match          100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 6
US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 65
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-65

Query Match          100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 7
US-09-867-847-1
; Sequence 1, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-1

Query Match          100.0%; Score 217; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-09-956-625-26
; Sequence 26, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-625-26
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Query Match      100.0%; Score 217; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
    |
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9
US-09-731-460-1
; Sequence 1, Application US/09731460
; Patent No. US20020137112A1
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOJKIER-04302
; CURRENT APPLICATION NUMBER: US/09/731,460
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-731-460-1

Query Match      100.0%; Score 217; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
    |
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 10
US-10-076-708-7
; Sequence 7, Application US/10076708
; Patent No. US20020164657A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Satish
; APPLICANT: Rank, Kenneth
; TITLE OF INVENTION: Assays for Accessing Aa-Tau Aggregation
; FILE REFERENCE: 6322
; CURRENT APPLICATION NUMBER: US/10/076,708
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-708-7

Query Match      100.0%; Score 217; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
    |
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 11
US-10-051-496-1
; Sequence 1, Application US/10051496
; Publication No. US20020182660A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Kei-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-1-43)
; Abeta(1-41), Abeta(1-42) and Abeta(1-43)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kei-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC Compatibles
; OPERATING SYSTEM: Windows
; SOFTWARE: MS No. US20020182660A1epad
; CURRENT APPLICATION DATA: US/10/051,496
; APPLICATION NUMBER: US/10/051,496
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,854A
; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 60/183,407
; FILING DATE: 18-February-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Koenig, C. Frederick III
; REGISTRATION NUMBER: 29,662
; REFERENCE/DOCKET NUMBER: PBI-PT001.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-6400
; TELEFAX: (215) 568-6499
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 Amino Acid
; TYPE: Amino Acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; CELL TYPE: <Unknown>
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: <Unknown>
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 1:FROM 1 TO 43
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-051-496-1

Query Match      100.0%; Score 217; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
    |
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 12
US-10-217-459-1
; Sequence 1, Application US/10217459
```

; Publication No. US20030069445A1
; GENERAL INFORMATION:
; APPLICANT: AUDIA, James
; APPLICANT: HYSLOP, Paul
; APPLICANT: NISSEN, Jeffrey
; APPLICANT: THOMPSON, Richard
; APPLICANT: TUNG, Jay
; APPLICANT: TANNER, Laura
; TITLE OF INVENTION: BIOLOGICAL REAGENTS AND METHODS FOR DETERMINING THE
; FILE REFERENCE: 002010-354
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 09/164,390
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: beta-amyloid precursor protein
; US-10-217-459-1

Query Match 100.0%; Score 217; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 13
US-09-280-966-1
; Sequence 1, Application US/09280966
; Patent No. US20010020097A1
; GENERAL INFORMATION:
; APPLICANT: JAMES E. AUDIA
; BEVERLY K. FOLMER
; VARGHESE JOHN
; JEFFREY S. NISSEN
; WARREN J. PORTER
; EUGENE D. THORSETT
; JING WU
; TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL) AMINO
; ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
; COMPRISING SAME, AND METHODS FOR INHIBITING
; -AMYLOID PEPTIDE RELEASE AND/OR ITS

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,966
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,191
FILING DATE: 21 NOV 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 NOV 1996

ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 002010-335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-622-2300
; TELEFAX: 650-622-2499
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-280-966-1

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 14
US-09-904-987-1
; Sequence 1, Application US/09904987
; Patent No. US20020037908A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020037908Alactyl, Inc.
; TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prep
; TITLE OF INVENTION: Protein Assembly or Aggregation
; FILE REFERENCE: 42108/26146
; CURRENT APPLICATION NUMBER: US/09/904,987
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4
; DATABASE ENTRY DATE: 2000-09-15
; RELEVANT RESIDUES: (672)..(714)
; US-09-904-987-1

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 15
US-09-808-037-3
; Sequence 3, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match      100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. NO. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
    |||||||||||||||||||||||||||||||||||||||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

Search completed: April 21, 2003, 12:08:28
Job time : 15 secs
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:10 ; Search time 11.6667 Seconds
(without alignments)
82.401 Million cell updates/sec

Title: US-09-580-018-9

Perfect score: 10

Sequence: 1 DAEFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	5	2 A26830	mitosis inhibiting
2	3	30.0	7	2 PT0283	Ig heavy chain CRD
3	3	30.0	8	2 S78036	ribosomal protein
4	3	30.0	9	2 P10139	carbon-monoxide de
5	3	30.0	10	2 A59272	peptide-N4-(N-acet
6	3	30.0	10	2 PT0243	Ig heavy chain CRD
7	3	30.0	10	2 PH0900	T-cell receptor be
8	2	20.0	3	3 PT0571	T-cell receptor be
9	2	20.0	4	2 S09478	globulin IV alpha
10	2	20.0	4	2 PT0633	T-cell receptor be
11	2	20.0	4	2 PT0711	T-cell receptor be
12	2	20.0	4	2 PT0698	T-cell receptor be
13	2	20.0	4	2 PT0677	T-cell receptor be
14	2	20.0	4	2 PT0706	T-cell receptor be
15	2	20.0	4	2 PT0675	T-cell receptor be
16	2	20.0	4	2 PT0566	T-cell receptor be
17	2	20.0	5	2 C23751	spinal cord peptid
18	2	20.0	5	2 A41225	copper resistance
19	2	20.0	5	2 B41225	copper resistance
20	2	20.0	5	2 D60274	major protein anti
21	2	20.0	5	2 B37988	acid proteinase li
22	2	20.0	5	2 A44692	fulicin - giant Af
23	2	20.0	5	2 J70520	Ig kappa chain V-I
24	2	20.0	5	2 D44823	Synaptosomal-assoc
25	2	20.0	5	2 PT0596	T-cell receptor be
26	2	20.0	5	2 PT0513	T-cell receptor be
27	2	20.0	5	2 PT0600	T-cell receptor be
28	2	20.0	5	2 PT0608	T-cell receptor be
29	2	20.0	5	2 PT0669	T-cell receptor be

30 2 20.0 5 2 PT0553 T-cell receptor be
31 2 20.0 5 2 PT0538 T-cell receptor be
32 2 20.0 5 2 PT0540 T-cell receptor be
33 2 20.0 5 2 PT0703 T-cell receptor be
34 2 20.0 5 2 PT0690 T-cell receptor be
35 2 20.0 5 2 PT0707 T-cell receptor be
36 2 20.0 5 2 PT0573 T-cell receptor be
37 2 20.0 5 2 PT0572 T-cell receptor be
38 2 20.0 5 2 PT0679 T-cell receptor be
39 2 20.0 5 2 PT0701 T-cell receptor be
40 2 20.0 5 2 PT0717 T-cell receptor be
41 2 20.0 6 2 S02617 alcohol dehydrogen
42 2 20.0 6 2 A61411 ameleitin - rat
43 2 20.0 6 2 JU0355 lipopeptide WS1279
44 2 20.0 6 2 S29637 jacalin beta-II ch
45 2 20.0 6 2 A60494 antineoplastic gly

ALIGNMENTS

RESULT 1

A26830 mitosis inhibiting peptide - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: A26830

R:Reichelt, K.; Elgjo, K.; Edminson, P.D.

Biochem. Biophys. Res. Commun. 145, 1493-1501, 1987

A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.

A:Reference number: A26830; MUID:87298602; PMID:3619940

A:Accession: A26830

A:Molecule type: protein

A:Residues: 1-5 <REI>

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; pyroglutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSG 9

Db 3 DSG 5

RESULT 2

PT0283

Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0283

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0283

A:Molecule type: DNA

A:Residues: 1-7 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAE 3

Db 1 DAE 3

RESULT 3

S78036
ribosomal protein YmS-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C:Species: Saccharomyces cerevisiae
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C:Accession: S78036
R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma
Eur. J. Biochem. 245, 449-456, 1997
A:Title: Identification and characterization of the genes for mitochondrial ribosomal pr
A:Reference number: S78018; MUID:97796414; PMID:9151978
A:Accession: S78036
A:Molecule type: protein
A:Residues: 1-8 <KIT>
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSG 9
DB 6 DSG 8

RESULT 4
PL0139
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr
C:Species: Pseudomonas carboxydoflava
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0139
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotro
A:Reference number: PL0138; MUID:90055678; PMID:2818128
A:Accession: PL0139
A:Molecule type: protein
A:Residues: 1-9 <KRA>
A:Note: 2-Net is also found
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C:Keywords: oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAE 3
DB 7 DAE 9

RESULT 5
A59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain
N:Alternate names: peptide N-glycosidase
C:Species: Prunus dulcis var. sativa (sweet almond)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C:Accession: A59272
R:Altmann, F.; Paschinger, K.; Dalik, T.; Voraauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A:Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A:Reference number: A59272; MUID:98181894; PMID:9523720
A:Accession: A59272
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ALT>
C:Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGY 10
DB 3 SGY 5

RESULT 6
PT0243
Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0243
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0243
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGY 10
DB 7 SGY 9

RESULT 7
PH0900
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0900
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0900
A:Molecule type: mRNA
A:Residues: 1-10 <GOL>
A:Experimental source: myelin basic protein-immunized T-cell
C:Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSG 9
DB 5 DSG 7

RESULT 8
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PT0571
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0571
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-3 <FEF>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9
||
Db 2 SG 3

RESULT 9

S09478 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)

N;Alternate names: IIS globulin alpha subunit gamma chain

C;Species: Cucurbita sp. (cucurbit)

C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996

C;Accession: S09478

R;Ohmura, M.; Hara, I.; Matsubara, H.

Plant Cell Physiol. 21, 157-167, 1980

A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and

A;Reference number: S09066

A;Molecule type: protein

A;Residues: 1-4 <OHM>

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GY 10
||
Db 3 GY 4

RESULT 10

PT0633

T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0633

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0633

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9
||
Db 2 SG 3

RESULT 11

PT0711

T-cell receptor beta chain V-D-J region (120-2I) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0607

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <FEI>

A;Experimental source: newborn thymus, strain BALB/c, 120-2J

A;Accession: PT0674

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9
||
Db 2 SG 3

RESULT 12

PT0698

T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997

C;Accession: PT0546; PT0698; PT0583

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0546

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH

A;Accession: PT0698

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <FE2>

A;Experimental source: newborn thymus, strain BALB/c, 135-1BP

A;Accession: PT0583

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <FE3>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C

C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9
||
Db 3 SG 4

RESULT 13

PT0677

T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0558; PT0677

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0558

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG

A:Accession: PT0677

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SG 9

||

Db 2 SG 3

RESULT 14

PT0706

T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0706

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0706

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SG 9

||

Db 2 SG 3

RESULT 15

PT0675

T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0675

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0675

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SG 9

||

Db 2 SG 3

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:25 ; Search time 6.33333 Seconds
(without alignments)
65.489 Million cell updates/sec

Title: US-09-580-018-9
Perfect score: 10
Sequence: 1 DAEFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2	20.0	1 RE2L_LITRU	P82071 litoria rub
2	2	20.0	1 RE3L_LITRU	P82072 litoria rub
3	2	20.0	5 1 UXM4_CHLTR	P38005 chlamydia t
4	2	20.0	6 1 FARP_MONEX	P41966 moniezia ex
5	2	20.0	6 1 TRPI_PSEPU	P36414 pseudomonas
6	2	20.0	1 UN06_CLOPA	P81351 clostridium
7	2	20.0	7 1 FAP1_ASCSU	P31889 ascaris suu
8	2	20.0	7 1 UF03_MOUSE	P38641 mus musculus
9	2	20.0	8 1 ALI7_CARMA	P81820 carcinus ma
10	2	20.0	8 1 ALL5_CYDPO	P82156 cydia pomon
11	2	20.0	8 1 CPD1_ENTFA	P13269 enterococcu
12	2	20.0	8 1 GLUR_HUMAN	P02729 homo sapien
13	2	20.0	8 1 LCK4_LEUMA	P21143 leucophaea
14	2	20.0	8 1 LCK5_LEUMA	P19987 leucophaea
15	2	20.0	8 1 ORNY_ORCLI	P82455 orconectes
16	2	20.0	8 1 PPK3_PERAM	P82618 periplaneta
17	2	20.0	8 1 UC26_MAIZE	P80632 zea mays (m
18	2	20.0	8 1 VGLG_HSV2B	P81780 herpes simp
19	2	20.0	9 1 COXE_THUOB	P80975 thunnus obe
20	2	20.0	9 1 DSIP_RABIT	P01158 oryctolagus
21	2	20.0	9 1 FAP5_ASCSU	P43170 ascaris suu
22	2	20.0	9 1 FAP6_CALVO	P41861 calliphora
23	2	20.0	9 1 FARP_CALSI	P38495 callinectes
24	2	20.0	9 1 FIBB_MACFU	P19345 macaca fusc
25	2	20.0	9 1 FIBB_PAPAN	P19344 papio anubi
26	2	20.0	9 1 IPYR_RHOVI	P82992 rhodopseudo
27	2	20.0	9 1 MOSF_GLYJA	P19853 glypeaster
28	2	20.0	9 1 MOSH_GLYJA	P19852 glypeaster
29	2	20.0	9 1 NEUU_CAVPO	P34966 cavia porce
30	2	20.0	9 1 NEUX_HUMAN	P04277 homo sapien
31	2	20.0	9 1 OXYT_OCTVU	P80027 octopus vul
32	2	20.0	9 1 TKL1_LOCFI	P16223 locusta mig
33	2	20.0	9 1 TRP4_LEUMA	P81736 leucophaea

34 2 20.0 9 1 XILA_STRSQ P19149 streptomycete
35 2 20.0 10 1 COXO_THDOB P80982 thunnus obe
36 2 20.0 10 1 COXQ_RABIT P80336 oryctolagus
37 2 20.0 10 1 CU30_LOCFI P11735 locusta mig
38 2 20.0 10 1 ESTA_SCHGA P81012 schizaphis
39 2 20.0 10 1 FARP_MYTED P42560 mytilus edu
40 2 20.0 10 1 FIBB_CERSI P14537 ceratotheri
41 2 20.0 10 1 GAJU_HUMAN P01358 homo sapien
42 2 20.0 10 1 GLEM_HUMAN P20738 petromyzon
43 2 20.0 10 1 GON3_PETMA P30948 petromyzon
44 2 20.0 10 1 HTF_HELZE P16353 heliothis z
45 2 20.0 10 1 HTF_TABAT P14596 tabanus atr

ALIGNMENTS

RESULT 1

RE2L_LITRU ID RE2L_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 2.1.
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC -!- ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EF 4

Db 2 EF 3

RESULT 2

RE3L_LITRU ID RE3L_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog
 RT 'litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 ACTIVITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.

KW Amphibian skin; Amidation.

FT MOD_RES 5 5 AMIDATION.

SQ SEQUENCE 5 AA: 656 MW; 71A9C9CBLU3000000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 EF 4

Db 2 EF 3

RESULT 3

UXA4_CHLTR

ID UXA4_CHLTR STANDARD; PRT; 5 AA.

AC P38005;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Unknown protein from 2D-page from elementary body (Fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE.

RC STRAIN=L2/434/Bu;

RA Bin L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

RA Comanducci M., Christensen G., Birkelund S., Vitreou E., Ratti G.,

RA Pallini V.;

RL Submitted (SEP-1994) to the SWISS-PROT data bank.

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 4.5 ITS MW IS: 28 kDa.

DR Slena-ZDPAGE; P38005; -.

FT NON_TER 5

SQ SEQUENCE 5 AA: 474 MW; 75BAAB65AA8000000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 SG 9

Db 2 SG 3

RESULT 4

FARP_MONEX

ID FARP_MONEX STANDARD; PRT; 6 AA.

AC P41966;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FMRamide-like neuropeptide GNFRP-amide.

OS Moniezia expansa (Sheep tapeworm).

OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;

OC Cyclophyllidae; Anoplocephalidae; Moniezia.

OX NCBI_TaxID=28841;

RN [1]

RP SEQUENCE.

RX MEDLINE=93312289; PubMed=8323531;

RA Maule A.G., Shaw C., Halton D.W., Thim L.;

RA "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from

RT the sheep tapeworm, Moniezia expansa.";

RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 6 6 AMIDATION.

SQ SEQUENCE 6 AA: 787 MW; 69D409C9C4481000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 6;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 FR 5

Db 4 FR 5

RESULT 5

TRPL_PSEPU

ID TRPL_PSEPU STANDARD; PRT; 6 AA.

AC P36414;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE TrpBA operon transcriptional activator (Fragment).

GN TRPI.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PPG1 C1S;

RX MEDLINE=89335926; PubMed=2503057;

RA Eberly L., Crawford I.P.;

RT "DNA sequence of the tryptophan synthase genes of Pseudomonas

putida.";

RL Biochimie 71:521-531(1989).

CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE

TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

REGULATORS.

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 or send an email to license@isb-sib.ch).

CC EMBL; X13299; CAA31660.1; -.

DR InterPro; IPR000847; HTH_LYSR.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.

KW Tryptophan biosynthesis; Transcription regulation; Activator;

KN DNA-binding.

FT NON_TER 6 6

SQ SEQUENCE 6 AA: 683 MW; 77672AA1EDD6F000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 6;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 HD 7

Db 3 HD 4

RESULT 6

UN06_CLOPA

ID UN06_CLOPA STANDARD; PRT; 6 AA.

AC P81351;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AE 3
 DB 4 AE 5
 RESULT 7
 ID FARL_ASCSU STANDARD; PRT; 7 AA.
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PMRFamide-like neuropeptide AF1.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AF1, a sequenced bioactive neuropeptide isolated from the nematode
 RT Ascaris suum";
 RL Neuron 2:1465-1473(1989).
 CC -I- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE
 CC INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CC CELLS.
 CC -I- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -I- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EF 4
 DB 3 EF 4
 RESULT 8
 ID UF03_MOUSE STANDARD; PRT; 7 AA.
 AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AE 3
 DB 4 AE 5
 RESULT 9
 ID AL17_CARMA STANDARD; PRT; 8 AA.
 AC P81820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 17.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Cerebral ganglion; Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestri J.L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 SG 9
 DB 1 SG 2
 RESULT 10
 ID AL15_CYDPO STANDARD; PRT; 8 AA.
 AC P82156;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE Cydiastatin 5.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GY 10
Db 3 GY 4

RESULT 11
CPDL_ENTFA
ID CPDL_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPDL.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040389; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, CPDL.";
RL Science 226:849-850(1984).
CC -|- FUNCTION: CPDL IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPDL.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9
Db 7 SG 8

RESULT 12
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25p-25p(1971).
CC -|- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GAL. .).
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HD 7
Db 5 HD 6

RESULT 13
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -|- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -|- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DA 2
Db 1 DA 2

RESULT 14
LCK5_LEUMA
ID LCK5_LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.

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OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp Biochem Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LECOKININS.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SG 9
DB 2 SG 3

RESULT 15
ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomyotropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Astacoidea; Astacoidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdick S., Sauter A., Keller R.;
RT "Two orconekins and the novel octapeptide orcomyotropin in the hindgut
RT of the crayfish Orconectes limosus: identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion.";
RL J. Exp. Biol. 203:2807-2818(2000).
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
CC BY ABDOMINAL GANGLIONIC NEURONS.
CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DA 2
DB 2 DA 3

Search completed: April 21, 2003, 12:10:27
Job time : 6.33333 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run On: April 21, 2003, 12:07:50 ; Search time 22 Seconds
(without alignments)
93.658 Million cell updates/sec

Title: US-09-580-018-9
Perfect score: 10
Sequence: 1 DAEFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	13 Q9PS69	Q9PS69 gallus gall
2	3	30.0	9	2 P72149	P72149 pseudomonas
3	3	30.0	10	6 Q9TU33	Q9TU33 canis famil
4	3	30.0	10	10 P81899	P81899 prunus dulc
5	3	30.0	10	12 Q9JIG8	Q9JIG8 tt virus. o
6	2	20.0	7	2 Q47477	Q47477 escherichia
7	2	20.0	7	4 Q15897	Q15897 homo sapien
8	2	20.0	7	6 Q28742	Q28742 oryctolagus
9	2	20.0	7	8 Q98866	Q98866 spinacia ol
10	2	20.0	7	11 O55184	O55184 rattus norv
11	2	20.0	8	2 O68485	O68485 klebsiella
12	2	20.0	8	2 Q9X3K1	Q9X3K1 prochloroco
13	2	20.0	8	2 Q9S6D5	Q9S6D5 escherichia
14	2	20.0	8	2 P72221	P72221 pseudomonas
15	2	20.0	8	2 Q9R7T2	Q9R7T2 escherichia
16	2	20.0	8	2 P83152	P83152 anabaena sp

17	2	20.0	8	2	Q9RSK2	Q9RSK2 shigella dy
18	2	20.0	8	2	Q9R3X0	Q9R3X0 planktothri
19	2	20.0	8	2	Q9RS17	Q9RS17 clostridium
20	2	20.0	8	2	Q8RSR3	Q8RSR3 lactobacilli
21	2	20.0	8	3	Q9URB9	Q9URB9 saccharomyc
22	2	20.0	8	4	Q15901	Q15901 homo sapien
23	2	20.0	8	4	Q9Y4J4	Q9Y4J4 homo sapien
24	2	20.0	8	4	Q16428	Q16428 homo sapien
25	2	20.0	8	4	O60773	O60773 homo sapien
26	2	20.0	8	5	Q9UB13	Q9UB13 albinaria h
27	2	20.0	8	5	Q94623	Q94623 manduca sex
28	2	20.0	8	5	P82686	P82686 periplaneta
29	2	20.0	8	6	Q9MYL5	Q9MYL5 pongo pygma
30	2	20.0	8	6	Q9GMH3	Q9GMH3 lagenorhync
31	2	20.0	8	6	Q28866	Q28866 megaptera n
32	2	20.0	8	6	Q8WNS1	Q8WNS1 bos taurus
33	2	20.0	8	6	Q9BFC3	Q9BFC3 didelphis m
34	2	20.0	8	6	Q9BFC2	Q9BFC2 macropus eu
35	2	20.0	8	6	Q9BFC1	Q9BFC1 choloepus h
36	2	20.0	8	6	Q9BFC0	Q9BFC0 choloepus d
37	2	20.0	8	6	Q9BFB9	Q9BFB9 euphractus
38	2	20.0	8	6	Q9BFB8	Q9BFB8 chaetophrac
39	2	20.0	8	6	Q9BFB7	Q9BFB7 tamandua te
40	2	20.0	8	6	Q9BFB6	Q9BFB6 myrmecophag
41	2	20.0	8	6	Q9BFB5	Q9BFB5 erinaceus c
42	2	20.0	8	6	Q9BFB4	Q9BFB4 talpa alta
43	2	20.0	8	6	Q9BFB3	Q9BFB3 condylura c
44	2	20.0	8	6	Q9BFB2	Q9BFB2 sorex arane
45	2	20.0	8	6	Q9BFB1	Q9BFB1 echinops te

ALIGNMENTS

RESULT 1

Q9PS69 PRELIMINARY; PRT; 8 AA.
AC Q9PS69; DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;

Query Match 30.0%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSG 9
Db 2 DSG 4

RESULT 2

P72149 PRELIMINARY; PRT; 9 AA.
ID P72149
AC P72149;
DT 01-FEB-1997 (TREMBLrel. 02, Created)

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DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative glucokinase (Fragment).
GN GLK.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PA01;
RX MEDLINE=96427344; PubMed=8830708;
RA Sage A.E., Proctor W.D., Phibbs P.V.Jr.;
RT "A two-component response regulator, gltr, is required for glucose
RT transport activity in Pseudomonas aeruginosa PA01.";
RL J. Bacteriol. 178:6064-6066(1996).
DR EMBL; U50932; AAC44474.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 944 MW; C3071DDAA72DC6C6 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAE 3
Db 6 DAE 8

RESULT 3
Q9TU33
ID Q9TU33 PRELIMINARY; PRT; 10 AA.
AC Q9TU33;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BRCA1 (Fragment).
GN BRCA1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20154965; PubMed=10690375;
RA Gray I.S., Yuzbasilyan-Gurkan V.;
RT "A single nucleotide (T-->G) polymorphism within intron 23 of the
RT canine BRCA1 gene.";
RL Anim. Genet. 31:76-77(2000).
DR EMBL; AF159258; AAD56289.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65B8AAB01B3 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSG 9
Db 6 DSG 8

RESULT 4
P81899
ID P81899 PRELIMINARY; PRT; 10 AA.
AC P81899;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large
DE chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
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DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX PubMed=9523720;
RA Altmann F., Paschinger K., Dalik T., Vorauer K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT amidase A and its N-glycans.";
RL Eur. J. Biochem. 252:118-123(1998).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -!- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -!- MASS SPECTROMETRY: MW=54182; METHOD=MALDI-MS.
KW Hydrolase; Glycoprotein.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGY 10
Db 3 SGY 5

RESULT 5
Q9JIG8
ID Q9JIG8 PRELIMINARY; PRT; 10 AA.
AC Q9JIG8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -.
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEF 4
Db 2 AEF 4

RESULT 6
Q47477
ID Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
```



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DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellenga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
DB 1 AE 2

RESULT 7
Q15897 PRELIMINARY; PRT; 7 AA.
ID Q15897
AC Q15897
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (clone XP6A11A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 20.0%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
DB 5 AE 6

RESULT 8
Q28742 PRELIMINARY; PRT; 7 AA.
ID Q28742
AC Q28742
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).

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OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 20.0%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HD 7
DB 4 HD 5

RESULT 9
O98866 PRELIMINARY; PRT; 7 AA.
ID O98866
AC O98866
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sjibben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 20.0%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FR 5
DB 2 FR 3

RESULT 10
O55184 PRELIMINARY; PRT; 7 AA.
ID O55184
AC O55184
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Orphan receptor TR4-NS (Fragment).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

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RN  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY;
RX  MEDLINE=96198747; PubMed=8612486;
RA  Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA  Detera-Wadleigh S.D.;
RT  "Splice variants of rat TR4 orphan receptor: differential expression
RT  of novel sequences in the 5'-untranslated region and C-terminal
RT  domain.";
RL  Endocrinology 137:1562-1571(1996).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY;
RX  MEDLINE=96299786; PubMed=8661150;
RA  Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT  "New variants of the human and rat nuclear hormone receptor, TR4:
RT  expression and chromosomal localization of the human gene.";
RL  Genomics 35:361-366(1996).
DR  EMBL; U59454; AAB91433.1; -.
KW  Receptor.
FT  NON_TER 1
SQ  SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 20.0%; Score 2; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DA 2
Db 6 DA 7

RESULT 11
O68485
ID 068485 PRELIMINARY; PRT; 8 AA.
AC 068485;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
GN ADAL
OS Klebsiella pneumoniae.
OG Plasmid pLQ1000.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98287600; PubMed=9624504;
RA Centron D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT aac(6')-Iq from the integron of a natural multiresistance plasmid.";
RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
DR EMBL; AF047556; AAC25501.1; -.
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
Db 3 AE 4

RESULT 12
Q9X3K1
ID Q9X3K1 PRELIMINARY; PRT; 8 AA.
AC Q9X3K1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070193; AAD23233.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SG 9
Db 5 SG 6

RESULT 13
Q9S6D5
ID Q9S6D5 PRELIMINARY; PRT; 8 AA.
AC Q9S6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Putative IS30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Rahn A., Drummel-Smith J., Whitfield C.;
RT "Conserved organization in the cps gene clusters for expression of
RT Escherichia coli group 1 k antigens: relationship to the colanic acid
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
Db 7 AE 8

RESULT 14
P72221
ID P72221 PRELIMINARY; PRT; 8 AA.
AC P72221;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alginatase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;

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```
RN SEQUENCE FROM N.A.
RP STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=OS-ALG-9;
RX MEDLINE=93329366; PubMed=8336113;
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an alginate lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38469; BAA21704.1; -.
KW Lyase.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
Db 7 AE 8

RESULT 15
Q9R7T2 PRELIMINARY; PRT; 8 AA.
AC Q9R7T2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN Y0FG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-Kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996).
DR EMBL; D90705; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AE 3
Db 5 AE 6
```


GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 11:57:04 ; Search time 36 seconds
(without alignments)
155.459 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAERHDGSGVEVHHQKLVFF.....DVGSNKGAIGLMGVGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_101002.*
- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 - 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 - 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 - 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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 - 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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 - 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	42	13	Sequence of A99 (b
2	217	100.0	42	15	Beta-amyloid (1-42
3	217	100.0	42	17	Beta/A4-amyloid pe
4	217	100.0	42	17	Alzheimer amyloid
5	217	100.0	42	18	Beta A4 peptide.
6	217	100.0	42	19	Neurotoxic beta-am
7	217	100.0	42	19	Beta-amyloid pepti
8	217	100.0	42	19	Full length beta-a
9	217	100.0	42	20	Human beta amyloid
10	217	100.0	42	20	Human amyloidogeni

11	217	100.0	42	20	AA25137	Human amyloid beta
12	217	100.0	42	20	AA25137	Human beta-amyloid
13	217	100.0	42	20	AA25137	A-beta-binding pep
14	217	100.0	42	20	AA25137	Mutant aggregating
15	217	100.0	42	20	AA25137	Human tachykinin a
16	217	100.0	42	20	AA25137	Synthetic amyloid
17	217	100.0	42	20	AA25137	Beta-amyloid 1-42
18	217	100.0	42	22	AA25137	Amyloid-beta pepti
19	217	100.0	42	22	AA25137	Human peptide anti
20	217	100.0	42	22	AA25137	Human Alzheimer-be
21	217	100.0	42	22	AA25137	Amyloid beta-prote
22	217	100.0	42	22	AA25137	Amyloid beta-prote
23	217	100.0	42	22	AA25137	Human amyloid beta
24	217	100.0	42	22	AA25137	Human amyloid prot
25	217	100.0	42	22	AA25137	Human amyloid-beta
26	217	100.0	42	22	AA25137	Human amyloid pept
27	217	100.0	42	22	AA25137	Beta/A4-amyloid pe
28	217	100.0	42	23	AA25137	Human amyloid beta
29	217	100.0	42	23	AA25137	Amyloid-beta (Abet
30	217	100.0	42	23	AA25137	Human Amyloid beta
31	217	100.0	42	23	AA25137	Amyloid precursor
32	217	100.0	42	23	AA25137	Human beta-amyloid
33	217	100.0	42	23	AA25137	Beta amyloid pepti
34	217	100.0	42	23	AA25137	Human beta-amyloid
35	217	100.0	42	23	AA25137	Amino acids 1-42 o
36	217	100.0	42	23	AA25137	Human amyloid beta
37	217	100.0	42	23	AA25137	Human beta amyloid
38	217	100.0	42	23	AA25137	Neuronal death inh
39	217	100.0	42	23	AA25137	Amyloid peptide pr
40	217	100.0	43	10	AA25137	Region of pre-APC
41	217	100.0	43	15	AA25137	Beta amyloid pepti
42	217	100.0	43	15	AA25137	Beta-amyloid (1-43
43	217	100.0	43	15	AA25137	Amyloid beta-prote
44	217	100.0	43	16	AA25137	Beta amyloid prote
45	217	100.0	43	17	AA25137	A-beta protein (43

ALIGNMENTS

RESULT 1
AAR20330
ID AAR20330 standard; peptide; 42 AA.
XX AC AAR20330;
XX AC AAR20330;
DT 14-APR-1992 (first entry)
XX Sequence of A99 (beta-amyloid core domain).
DE Transgenic mice; Alzheimer's disease; diagnosis;
KW beta-amyloid precursor; plaque core protein.
XX Homo sapiens.
XX WO9119810-A.
XX 26-DEC-1991.
XX 17-JUN-1991; 91WO-US04447.
XX 15-JUN-1990; 90US-0538857.
XX (CALB-) CALIF BIOTECHN INC.
XX Cordell B;
XX WPI; 1992-024426/03.
XX Transgenic mice as models for studying Alzheimer's disease
XX proteins - contg. cells with promoter and beta-amyloid precursor
XX protein deoxyribonucleic acid, useful for testing
XX anti-alzheimer's drugs

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XX PS Disclosure; Fig 3; 98pp; English.
XX CC
XX CC The inventors specifically claim transgenic mice contg. DNA encoding
XX CC A42 (beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid
XX CC carboxy tail) (AAR20329), A695 (beta-amyloid precursor protein), A751
XX CC (precursor plus inhibitor) or A41 (protease inhibitor) (AAR20328).
XX CC Human fibroblast cDNA clone lambdaARCP16814 was deposited at ATCC on
XX CC July 1, 1987 and has accession No. 40347. The promoter is pref. the
XX CC NSE promoter with the A751 or the A695 sequence.
XX SQ Sequence 42 AA;
Query Match 100.0%; Score 217; DB 13; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
RESULT 2
AAR60366
ID AAR60366 standard; peptide; 42 AA.
XX AC AAR60366;
XX DT 15-MAR-1995 (first entry)
XX DE Beta-amyloid (1-42).
XX KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
XX KW anti-beta-amyloid antibody; diagnosis.
XX OS Homo sapiens.
XX PN WO9417197-A.
XX PD 04-AUG-1994.
XX PF 24-JAN-1994; 94WO-JP00089.
XX PR 25-JAN-1993; 93JP-0010132.
XX PR 05-FEB-1993; 93JP-0019035.
XX PR 16-NOV-1993; 93JP-0286985.
XX PR 28-DEC-1993; 93JP-0334773.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Kitada C, Odaka A, Suzuki N;
XX WPI; 1994-264110/32.
XX DT
XX PT Antibodies recognising specific parts of beta-amyloid - can be
XX PT used for diagnosis of diseases implicating beta-amyloid, such as
XX PT Alzheimer's disease
XX PS Disclosure; Page 83; 116pp; Japanese.
XX CC Antibodies which recognise specific subfragments of the beta-amyloid
XX CC protein are claimed. Specifically, the antibodies (which are pref.
XX CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
XX CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
XX CC from the C-terminal portion. The antibodies are useful for assaying
XX CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
XX CC disease.
XX SQ Sequence 42 AA;
Query Match 100.0%; Score 217; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
RESULT 3
AAR95248
ID AAR95248 standard; peptide; 42 AA.
XX AC AAR95248;
XX DT 20-JAN-1997 (first entry)
XX DE Beta/A4-amyloid peptide.
XX KW Beta/A4-amyloid peptide; tissue plasminogen activator;
XX KW Alzheimer's disease; stimulation; investigation; pathogenesis;
XX KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
XX KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
XX KW haemorrhage.
XX OS Homo sapiens.
XX PN WO9615799-A1.
XX PD 30-MAY-1996.
XX PF 22-NOV-1995; 95WO-US15007.
XX PR 22-NOV-1994; 94US-0347144.
XX PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX PI Anderson S;
XX WPI; 1996-268332/27.
XX DT
XX PT Use of agents which bind beta-amyloid peptide - for diagnosis,
XX PT prevention and treatment of vascular damage caused by amyloid
XX PT deposits, partic. in haemorrhaging and Alzheimer's disease
XX PS Example 1; Fig 1; 52pp; English.
XX CC To investigate the effects of beta-amyloid peptide (BAP) on
XX CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
XX CC One peptide contained 42 amino acids and corresp. to the full
XX CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
XX CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
XX CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
XX CC (HCHWA-D), respectively. In an assay to determine the effect of
XX CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
XX CC gave 1st order rate constant of activation (k(app)) values of
XX CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
XX CC and fibrinogen controls. The results demonstrate that the BAP are
XX CC able to stimulate t-PA activity in vitro, which is significant in
XX CC that it provides a means for investigating and controlling the
XX CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
XX CC angiopathy related cerebral haemorrhage.
XX SQ Sequence 42 AA;
Query Match 100.0%; Score 217; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
RESULT 4
AAR94591
```

ID AAR94591 standard; peptide; 42 AA.
 XX AAR94591;
 XX
 DT 21-AUG-1996 (first entry)
 XX
 XX Alzheimer amyloid beta-protein active site sequence.
 XX
 KW Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;
 KW serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;
 KW complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.
 XX
 OS Synthetic.
 XX
 XX US5506097-A.
 XX
 XX 09-APR-1996.
 XX
 XX 24-AUG-1990; 90US-0572671.
 XX
 XX 10-JAN-1994; 94US-0179574.
 XX 24-AUG-1990; 90US-0572671.
 XX 13-JAN-1992; 92US-0819361.
 XX 13-JAN-1993; 93WO-US00325.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 XX Kayyali U, Potter H;
 XX
 XX WPI; 1996-200270/20.
 XX
 XX Inhibiting enzymatic activity of Alzheimer amyloid beta-protein -
 PT using p-amidino-phenylmethanesulphonyl fluoride or ebelactone A,
 PT for treatment, study and diagnosis of Alzheimer's disease, etc.
 XX
 XX Disclosure; Fig 1; 17pp; English.
 XX
 XX This is the sequence of a fragment of the beta-amyloid protein
 CC associated with Alzheimer's disease. The protein contains esterase
 CC (cholinesterase and lipase) activities based on active site similarities
 CC with serine proteases (see AAR94592-96). The esterase activity of the
 CC beta-amyloid protein is inhibited by the cpds. of the invention i.e.
 CC ebelactone A or para-amidinophenylmethanesulphonyl fluoride. Inhibition
 CC of these activities prevent complex formation between the beta-amyloid
 CC protein and alpha(1)-antichymotrypsin, thus can be used to treat, study
 CC or diagnose Alzheimer's or Down's diseases or normal ageing.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 217; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 5
 AAW12828
 ID AAW12828 standard; peptide; 42 AA.
 XX
 XX AAW12828;
 XX
 XX 08-DEC-1997 (first entry)
 XX
 XX Beta A4 peptide.
 XX
 XX Beta A4 peptide; Alzheimer's disease; peptide aggregation; brain;
 KW therapy; inhibitor.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO9707403-A1.
 XX
 XX 27-FEB-1997.
 XX
 XX 23-JUL-1996; 96WO-US12034.
 XX
 XX 16-AUG-1995; 95US-0515606.
 XX
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 XX Goyal S, Paul JW, Kiedel NG, Sahasrabudhe SR;
 XX
 XX WPI; 1997-165447/15.
 XX
 XX Determn. of the degree of betaA4 peptide aggregation using binding
 PT agent - used to screen cpds. for possible use in Alzheimer's disease
 PT treatment
 XX
 XX Disclosure; Page 10; 18pp; English.
 XX
 XX This sequence represents the beta A4 peptide. The degree of aggregation
 CC of this peptide is determined using the method of the invention. The beta
 CC A4 peptide is present in the brain of Alzheimer's disease patients, but
 CC not in the brain of non-Alzheimer's disease individuals. The peptide
 CC clumps or aggregates in the brain of Alzheimer's disease patients, where
 CC it may be responsible for the destruction of normal brain cells. Once the
 CC clumps or aggregates form, the formulation is almost irreversible. The
 CC method of the invention comprises reacting this sequence with a binding
 CC reagent capable of binding to it only in its non-aggregated state, to
 CC form an amount of a beta A4 peptide-bound reagent and an amount of
 CC protein free reagent. The amount of the beta A4 peptide, binding reagent
 CC complex is then measured. Compounds which inhibit aggregation of beta A4
 CC peptide are potentially useful for treatment of Alzheimer's disease.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 217; DB 18; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 6
 AAW64507
 ID AAW64507 standard; peptide; 42 AA.
 XX
 XX AAW64507;
 XX
 XX 20-OCT-1998 (first entry)
 XX
 XX Neurotoxic beta-amyloid peptide decoy peptide #20.
 XX
 XX Beta-amyloid peptide; beta-AP; neurotoxin; calcium influx;
 KW aggregate; Alzheimers disease; decoy; treatment.
 XX
 XX Synthetic.
 OS
 XX WO9830229-A1.
 XX
 XX 16-JUL-1998.
 XX
 XX 09-JAN-1998; 98WO-US00653.
 XX
 XX 29-OCT-1997; 97US-0960188.
 XX 10-JAN-1997; 97US-0035847.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX Blanchard BU, Ingram VM.
 XX

DR WPI: 1998-398795/34.
 XX Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor,
 PT useful for, e.g. treating Alzheimer's disease
 XX
 XX Example 8; Page 46; 68pp; English.
 XX
 CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
 CC form aggregates that increase calcium influx into neuronal cells. Such
 CC peptides can be used in the treatment of diseases associated with
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
 CC injection and orally, or from slow-release implants.
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42
 DB 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42
 RESULT 7
 AAW47230
 ID AAW47230 standard; peptide: 42 AA.
 XX
 AC AAW47230;
 XX
 DT 22-MAY-1998 (first entry)
 DE Beta-amyloid peptide residues 1-42.
 XX
 KW Screening assay; beta-amyloid peptide; treatment;
 KW amyloidosis disease; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN US5721106-A.
 XX
 PD 24-FEB-1998.
 XX
 PF 12-SEP-1994; 94US-0304585.
 XX
 PR 12-SEP-1994; 94US-0304585.
 PR 13-AUG-1991; 91US-0744767.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Maggio JE, Mantyh PW;
 XX
 DR WPI: 1998-168404/15.
 XX
 PT New in vitro screening assay for Alzheimer's disease drugs -
 PT comprises assessing binding of labelled beta-amyloid peptide to silk
 PT sample
 XX
 PS Claim 8; Columns 29-30; 36pp; English.
 XX
 CC The present sequence was used in the development of a novel in
 CC vitro screening assay for agents capable of affecting the
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method
 CC comprises contacting a silk sample with labelled BAP, optionally
 CC in the presence of a test agent, detecting the amount of label
 CC bound to the silk and assessing the effect of the agent on the
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are
 CC potentially useful for treating amyloidosis diseases, especially
 CC Alzheimer's disease.

XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42
 DB 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42
 RESULT 8
 AAW42989
 ID AAW42989 standard; peptide: 42 AA.
 XX
 AC AAW42989;
 XX
 DT 01-MAY-1998 (first entry)
 DE Full length beta-amyloid peptide (BAP).
 XX
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage.
 XX
 OS Homo sapiens.
 XX
 PN US5703209-A.
 XX
 PD 30-DEC-1997.
 XX
 PF 05-JUN-1995; 95US-0464248.
 XX
 PR 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI: 1998-076482/07.
 XX
 PT Amyloid precursor protein fusion polypeptides - comprising APP
 PT fragment and marker, useful for research and drug screening
 XX
 PS Disclosure; Column 7; 84pp; English.
 XX
 CC The present sequence represents a beta-amyloid peptide (BAP). Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16Lys and 17Leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
 CC APP-770. These isoforms are derived by alternative splicing. APP-APP 751
 CC is a deletion construct of APP-751, which has a deletion of 276 amino
 CC acids to within 15 amino acids of the BAP domain. APP can be used as a
 CC substrate for studying abnormal proteolytic cleavage which results in the
 CC release of BAP, and also to screen for drugs that will inhibit such
 CC cleavage.
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42
 DB 1 DAEFRHDSGYEVHQLVFFAEDVGSNGKAIIGLMVGGVIA 42

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9

AAAY49691
ID AAY49691 standard; peptide; 42 AA.

XX AC AAY49691;

XX DT 13-JAN-2000 (first entry)

XX DE Human beta amyloid precursor protein peptide.

XX KW Human; beta amyloid precursor protein; APP; beta secretase inhibition;
KW alpha secretase; neurological disorder; Alzheimer's disease;

XX KW Down's syndrome; mutation.

XX OS Homo sapiens.

XX PN WO9951752-A1.

XX PD 14-OCT-1999.

XX PF 31-MAR-1999; 99WO-JP01701.

XX PR 31-MAR-1998; 98JP-0101821.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Ozawa K, Ikeda S, Tabira T;

XX DR WPI; 1999-620208/53.

XX PT A cell line which produces beta amyloid precursor protein, used in the
PT investigation of neurological disorders such as Alzheimer's disease -

XX PS Disclosure; Page 41; 70pp; Japanese.

XX CC The present invention describes a cell line which produces beta amyloid
CC precursor protein (APP) and expresses alpha secretase activity but
CC expresses beta secretase activity only under an external stimulus.
CC Also described is a cloning method for DNA encoding beta secretase,
CC comprising: (1) inserting a DNA library into the cell line, expressing
CC the inserted DNA, and selecting cells expressing beta secretase then
CC isolating the beta secretase DNA from them; or (2) isolating nucleic
CC acid from the cell line with or without external stimulation and
CC performing subtractive cloning to identify DNA expressed only under
CC stimulation. Products from the present invention may be used in the
CC investigation of neurological disorders such as Alzheimer's disease
CC and Down's syndrome and in particular the association of mutations of
CC the beta APP with them. The present sequence represents a human
CC beta APP peptide.

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 10

AAAY33407
ID AAY33407 standard; peptide; 42 AA.

XX AC AAY33407;

XX DT 03-DEC-1999 (first entry)

XX DE Human amyloidogenic A-beta peptide 1.

XX KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW Down's Syndrome.

XX OS Homo sapiens.

XX PN WO9941279-A2.

XX PD 19-AUG-1999.

XX PF 12-FEB-1999; 99WO-US03231.

XX PR 13-FEB-1998; 98US-0074658.

XX PA (ARCH-) ARCH DEV CORP.

XX PI Lynn DG, Meredith SC, Burkoth TS;

XX DR WPI; 1999-561326/47.

XX PT Inhibiting amyloid plaque formation in humans suffering from
PT amyloidosis, Alzheimer's disease or Down's Syndrome -

XX PS Claim 21; Page 140; 141pp; English.

XX CC This invention describes a novel method for inhibiting amyloid
CC fibrillogenesis which comprises contacting tissue with a composition
CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC at an end terminal or a side chain, by conjugation to polyethylene
CC glycol, by conjugation to a second compound and a pharmaceutically
CC acceptable buffer, solvent or diluent. The methods are used to inhibit
CC amyloid plaque formation in humans suffering from amyloidosis,
CC Alzheimer's disease or Down's Syndrome. This sequence represents a
CC fragment of the beta-amyloid peptide described in the method of the
XX invention.

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 11

AAAY25137
ID AAY25137 standard; peptide; 42 AA.

XX AC AAY25137;

XX DT 26-AUG-1999 (first entry)

XX DE Human amyloid beta-A4 peptide 5.

XX KW Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
KW therapeutic drug; brain; Alzheimer's disease.

XX OS Homo sapiens.

XX PN US5919631-A.

XX PD 06-JUL-1999.

XX PF 17-JUL-1996; 96US-0682245.

XX PR 17-JUL-1996; 96US-0682245.

XX PA (HMRI) HOECHST MARION ROUSSEL INC.

PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 XX WPI; 1999-403957/34.
 DR Determination of degree of aggregation of a peptide, useful for
 XX identifying therapeutic drugs for treating Alzheimer's disease
 PT Claim 1; Column 7-8; 8pp; English.
 XX This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated
 CC (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to
 CC unaggregated (I); (b) measuring the amount of (II) bound to (I) to
 CC obtain a value (i); (c) repeating steps (a) and (b) with a second
 CC sample at a different time to obtain a second value (ii); and (d)
 CC determining the difference between (i) and (ii) which is inversely
 CC related to the degree of aggregation of (I). This method may be
 CC applied to a screen for compounds that inhibit aggregation of (I).
 CC These inhibitors may be used as therapeutic drugs to inhibit the
 CC formation of these aggregates in the brains of patients suffering
 CC from Alzheimer's disease.
 XX

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 |||||

RESULT 12
 AAY08607
 ID AAY08607 standard; Protein; 42 AA.
 AC AAY08607;
 XX 05-AUG-1999 (first entry)
 XX Human beta-amyloid precursor core protein A42.
 XX APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
 KW Alzheimer's disease; model; therapeutic compound; brain; mechanism;
 KW nerve tissue specific promoter; synthesis; inhibitor; deposition;
 KW plaque formation; treatment; A42.
 XX Homo sapiens.
 XX US5912410-A.
 PN 15-JUN-1999.
 PD 13-APR-1995; 95US-0422333.
 PF 21-OCT-1994; 94US-0327381.
 PR 15-JUN-1990; 90US-0538857.
 PR 17-JUN-1991; 91US-0716725.
 PR 13-APR-1995; 95US-0422333.
 XX (SCIO-) SCIOS INC.
 PA Cordell B;
 PI WPI; 1999-357231/30.
 XX Transgenic mice useful for studying compounds potentially useful in
 PT the treatment of Alzheimer's disease
 XX Disclosure; Fig 3; 72pp; English.
 PS

CC This invention describes novel transgenic mice expressing proteins
 CC related to the pathology of Alzheimer's disease and which provide models
 CC for studying potentially therapeutic compounds. The transgenic mice
 CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)
 CC and a nerve tissue specific promoter operably linked to the beta-APP
 CC allowing its expression to form beta-amyloid protein deposits in the
 CC animal's brain. The transgenic mouse is useful for elucidating the
 CC molecular mechanisms involved in the synthesis of and, more importantly,
 CC inhibiting the synthesis and deposition of beta-amyloid proteins (most
 CC importantly in the brain where plaque formation is associated with
 CC Alzheimer's disease) by inhibiting production and/or increasing cleavage
 CC after production. The transgenic animals provide useful models for
 CC studying the in vivo relationships of the proteins to each other and to
 CC other compounds being tested for their usefulness in treating Alzheimer's
 CC disease.
 XX

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 |||||

RESULT 13
 AAW29093
 ID AAW29093 standard; peptide; 42 AA.
 AC AAW29093;
 XX 20-JUL-1999 (first entry)
 XX A-beta-binding peptide 1-42.
 XX Cyclosporin; A-beta peptide; conjugate; neurological disease;
 KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
 KW ALS; non-immunosuppressive; amyloid plaque formation.
 XX Homo sapiens.
 XX WO9910374-A1.
 PN 04-MAR-1999.
 PD 25-AUG-1998; 98WO-US17544.
 PF 26-AUG-1997; 97US-0057751.
 PR (WISC) WISCONSIN ALUMNI RES FOUND.
 XX Rich DH, Solomon ME;
 XX WPI; 1999-276928/23.
 XX New A-beta-binding peptide conjugates and Csa analogs - useful in
 PT treatment of neurological diseases e.g. Alzheimer's disease,
 PT multiple sclerosis etc.
 XX Claim 5; Page 98; 129pp; English.
 XX New conjugates are disclosed which are of formula A-Z, in which: A is
 CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
 CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
 CC contiguous residues of A-beta peptide. The compounds are novel chemical
 CC inducers of dimerization which are non-immunosuppressive and which are
 CC inhibitors of A-beta peptide aggregation and deposition in amyloid
 CC plaques. The adverse consequences of amyloid plaque formation can be
 CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
 CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
 CC therefore providing a mechanism to minimize the amount of free A-beta

CC available for fibril formation and deposition. The compounds can be used
 CC for the treatment of Alzheimer's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.2e-25;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 14

AAW99585

ID AAW99585 standard; peptide; 42 AA.

XX AC AAW99585;

XX DT 22-JUN-1999 (first entry)

XX DE Mutant aggregating amyloid-beta peptide.

XX KW Aggregation; amyloid-beta peptide; fluorescent group; detection;

XX KW diagnosis; Alzheimer's disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9908695-A1.

XX PD 25-FEB-1999.

XX PF 13-AUG-1998; 98WO-US16809.

XX PR 14-AUG-1997; 97US-0055660.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Garzon-Rodriguez W, Glabe C;

XX DR WPI; 1999-190112/16.

XX PT New fluorescent labeled amyloid A-beta peptides

XX PS Example 1; Page 21; 50pp; English.

XX This sequence corresponds to a mutant aggregating amyloid-beta peptide
 CC which can be covalently labelled with a fluorescent group. The detection
 CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
 CC or detect a predisposition to Alzheimer's disease. The screening assays
 CC can be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid-beta peptide are also useful for exploring other aspects of
 CC amyloid structure.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.2e-25;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 15

AAW92726

ID AAW92726 standard; peptide; 42 AA.

XX

AC AAW92726;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #72.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX PN US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX PT Screening for neurotoxin inhibitors - by testing compounds for their
 effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 41-42; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.2e-25;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Search completed: April 21, 2003, 12:06:29

Job time : 38 secs

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RESULT 2
US-08-179-574-1
; Sequence 1, Application US/08179574
; Patent No. 5506097
; GENERAL INFORMATION:
; APPLICANT: Huntington Potter
; APPLICANT: Usamah Kayyali
; TITLE OF INVENTION: Compounds and Methods for Inhibiting
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/819,361
; FILING DATE: 13-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU90-03A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-179-574-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 3
US-08-347-144-1
; Sequence 1, Application US/08347144
; Patent No. 5589154
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-08-462-859A-19
; Sequence 19, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; USING SAME TO ACCESS AGENTS WHICH DOWN-REGULATE FORMATION
; OF B-AMYLOID PEPTIDE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-859A-19
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: STREET: One Campus Drive
: CITY: Parsippany
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07054
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,247A
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-683-2158
: TELEFAX: 201-683-4117
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-464-247A-19
:
: Query Match 100.0%; Score 217; DB 1; Length 42;
: Best Local Similarity 100.0%; Pred. No. 4e-26;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
QY 1 DAEFRHDSGVVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
: |||||
Db 1 DAEFRHDSGVVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
: |||||
:
RESULT 7
US-08-464-248A-19
: Sequence 19, Application US/08464248A
: Patent No. 5703209
: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: APPLICANT: Vitek, M. P.
: TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
: TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
: TITLE OF INVENTION: of B-Amyloid Peptide
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: American Cyanamid Company
: STREET: One Cyanamid Plaza
: CITY: Wayne
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07470-8426
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,248A
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)831-3246
: TELEFAX: (201)831-3305

```

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106

GENERAL INFORMATION:
APPLICANT: Magglo, John E.
APPLICANT: Manlyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 10
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: OAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106


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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-5

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 11
US-08-268-348A-1
; Sequence 1, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobeili, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-268-348A-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 12
US-08-433-734-2
; Sequence 2, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann W.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-734-2

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 13
US-08-609-090-9
; Sequence 9, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-9

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 14
US-07-737-371E-72
; Sequence 72, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEEX: 200154
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 15
US-08-422-333-4
; Sequence 4, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2436
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-422-333-4

```

Query Match	100.0%	Score 217;	DB 2;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 4e-26;		
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLYFFAEDVGSNKGAIIGLMWGVWIA 42
 |||||
Dd 1 DAEFRHDSGYEVHHQKLYFFAEDVGSNKGAIIGLMWGVWIA 42

Search completed: April 21, 2003, 12:08:07
Job time : 16 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:50 ; Search time 22 Seconds
(without alignments)

93.658 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAEFRHDSG 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SPTREMBL.21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	13 Q9PS69	Q9PS69 gallus gall
2	3	30.0	9	2 P72149	P72149 pseudomonas
3	3	30.0	10	6 Q9TU33	Q9TU33 canis famil
4	3	30.0	10	12 Q9J1G8	Q9J1G8 tt virus. o
5	2	20.0	7	2 Q47477	Q47477 escherichia
6	2	20.0	7	4 Q15897	Q15897 homo sapien
7	2	20.0	7	6 Q28742	Q28742 oryctolagus
8	2	20.0	7	8 Q98866	Q98866 spinacia ol
9	2	20.0	7	11 Q55184	Q55184 rattus norv
10	2	20.0	8	2 Q68485	Q68485 klebsiella
11	2	20.0	8	2 Q9X3K1	Q9X3K1 prochloroco
12	2	20.0	8	2 Q9S6D5	Q9S6D5 escherichia
13	2	20.0	8	2 P72221	P72221 pseudomonas
14	2	20.0	8	2 Q9R7T2	Q9R7T2 escherichia
15	2	20.0	8	2 P83152	P83152 anabaena sp
16	2	20.0	8	2 Q9R3X0	Q9R3X0 planktothri

17	2	20.0	8	2 Q9R5L7	Q9R5L7 clostridium
18	2	20.0	8	2 Q8RSR3	Q8RSR3 lactobacill
19	2	20.0	8	3 Q9URB9	Q9URB9 saccharomyc
20	2	20.0	8	4 Q15901	Q15901 homo sapien
21	2	20.0	8	4 Q9Y4J4	Q9Y4J4 homo sapien
22	2	20.0	8	4 Q16428	Q16428 homo sapien
23	2	20.0	8	4 Q60773	Q60773 homo sapien
24	2	20.0	8	5 Q9UBI3	Q9UBI3 albinaria h
25	2	20.0	8	5 Q94623	Q94623 manduca sex
26	2	20.0	8	5 P82686	P82686 periplaneta
27	2	20.0	8	5 Q9MYL5	Q9MYL5 pongo pygma
28	2	20.0	8	6 Q9GMH3	Q9GMH3 lagenorhync
29	2	20.0	8	6 Q28866	Q28866 megaptera n
30	2	20.0	8	6 Q8WNS1	Q8WNS1 bos taurus
31	2	20.0	8	6 Q9BFC3	Q9BFC3 didelphis m
32	2	20.0	8	6 Q9BFC2	Q9BFC2 macropus eu
33	2	20.0	8	6 Q9BFC1	Q9BFC1 choloepus h
34	2	20.0	8	6 Q9BFC0	Q9BFC0 choloepus d
35	2	20.0	8	6 Q9BFB9	Q9BFB9 euphractus
36	2	20.0	8	6 Q9BFB8	Q9BFB8 chaetophrac
37	2	20.0	8	6 Q9BFB7	Q9BFB7 tamandua te
38	2	20.0	8	6 Q9BFB6	Q9BFB6 myrmecophag
39	2	20.0	8	6 Q9BFB5	Q9BFB5 erinaceus c
40	2	20.0	8	6 Q9BFB4	Q9BFB4 talpa altai
41	2	20.0	8	6 Q9BFB3	Q9BFB3 condylura c
42	2	20.0	8	6 Q9BFB2	Q9BFB2 sorex arane
43	2	20.0	8	6 Q9BFB1	Q9BFB1 echinops te
44	2	20.0	8	6 Q9BFB0	Q9BFB0 trichechus
45	2	20.0	8	6 Q9BFA9	Q9BFA9 procavia ca

ALIGNMENTS

RESULT 1

Q9PS69 PRELIMINARY; PRT; 8 AA.
AC Q9PS69; DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stefani S., Barber D.L., Abersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;

Query Match 30.0%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DSG 10
DB 2 DSG 4

RESULT 2

P72149 PRELIMINARY; PRT; 9 AA.
ID P72149
AC P72149;
DT 01-FEB-1997 (TREMBlrel. 02, Created)

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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative glucokinase (Fragment).
GN GLK.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OC NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA MEDLINE=96427344; PubMed=8830708;
RA Sage A.E., Proctor W.D., Phibbs P.V.Jr.;
RT "A two-component response regulator, gltR, is required for glucose
RT transport activity in Pseudomonas aeruginosa PA01.";
RL J. Bacteriol. 178:6064-6066(1996).
DR EMBL; U50932; AAC44474.1; -.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 944 MW; C307IDDA72DC6C6 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAE 4
DB 6 DAE 8

RESULT 3
Q9TU33
ID Q9TU33 PRELIMINARY; PRT; 10 AA.
AC Q9TU33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BRCA1 (Fragment).
GN BRCA1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20154965; PubMed=10690375;
RA Gray I.S., Iuzbasiyan-Gurkan V.;
RT "A single nucleotide (T-->G) polymorphism within intron 23 of the
RT canine BRCA1 gene.";
RL Anim. Genet. 31:76-77(2000).
DR EMBL; AF159258; AAD56289.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DSG 10
DB 6 DSG 8

RESULT 4
Q9JIG8
ID Q9JIG8 PRELIMINARY; PRT; 10 AA.
AC Q9JIG8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF2.
OS TT virus.

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OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -.
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AEF 5
DB 2 AEF 4

RESULT 5
Q47477
ID Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDBD1DB0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
DB 1 AE 2

RESULT 6
Q15897
ID Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (clone XP6A11A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum Mol Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD03372046B0 CRC64;

Query Match 20.0%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
DB 5 AE 6

RESULT 7
Q28742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 20.0%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 HD 8
DB 4 HD 5

RESULT 8
O98866 PRELIMINARY; PRT; 7 AA.
AC O98866;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal

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RT protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 20.0%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FR 6
DB 2 FR 3

RESULT 9
O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Orphan receptor TR4-NS (Fragment).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.-Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 20.0%; Score 2; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DA 3
DB 6 DA 7

RESULT 10
O68485 PRELIMINARY; PRT; 8 AA.
AC O68485;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
GN ADAL.
OS Klebsiella pneumoniae.
OC Plasmid pIQ1000.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98287600; PubMed=9624504;
RA Centron D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT aac(6')-Iq from the integron of a natural multiresistance plasmid.";
RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
DR EMBL; AF047556; AAC25501.1; -.
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
DB 3 AE 4

RESULT 11
O9X3K1 PRELIMINARY; PRT; 8 AA.
AC O9X3K1;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070193; AAD23233.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
DB 5 SG 6

RESULT 12
O9S6D5 PRELIMINARY; PRT; 8 AA.
AC O9S6D5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Putative IS30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Rahn A., Drummelsmith J., Whitfield C.;

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RT "Conserved organization in the cps gene clusters for expression of
RT Escherichia coli group 1 K antigens: relationship to the colanic acid
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;

```

```

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 AE 4
DB 7 AE 8

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RESULT 13

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P72221 PRELIMINARY; PRT; 8 AA.
AC P72221;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Alginase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RX MEDLINE=93329366; PubMed=8336113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an alginase lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38459; BAA21704.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;

```

```

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 AE 4
DB 7 AE 8

```

RESULT 14

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Q9R7T2 PRELIMINARY; PRT; 8 AA.
AC Q9R7T2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (fragment).
GN YQFG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;

```



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RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996).
DR EMBL; D90705; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
Db 5 AE 6

RESULT 15
P83152
ID P83152 PRELIMINARY; PRT; 8 AA.
AC P83152;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Allophycocyanin beta chain (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_taxid=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILLIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
CC ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
KW Thylakoid; Membrane.
FT NON_TER 8
SQ SEQUENCE 8 AA; 788 MW; 87CDC1A05DDAB6DD CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DA 3
Db 3 DA 4

Search completed: April 21, 2003, 12:11:39
Job time : 24 secs
```


GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:25 ; Search time 6.33333 Seconds
(without alignments)
65.489 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAEFRHDSG 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2	20.0	5	1 RE21_LITRU	P82071 litoria rub
2	2	20.0	5	1 RE31_LITRU	P82072 litoria rub
3	2	20.0	5	1 UX44_CHLTR	P38005 chlamydia t
4	2	20.0	6	1 FARP_MONEX	P41966 moniezia ex
5	2	20.0	6	1 TRPI_PSEPU	P36414 pseudomonas
6	2	20.0	6	1 UN06_CLOPA	P81351 clostridium
7	2	20.0	7	1 FARI_ASCSU	P31889 ascaris suu
8	2	20.0	7	1 UF03_MOUSE	P38641 mus musculus
9	2	20.0	8	1 AL17_CARMA	P81820 carcinus ma
10	2	20.0	8	1 CCKN_MACEU	P30369 macropus eu
11	2	20.0	8	1 CPD1_ENTFA	P13269 enterococcu
12	2	20.0	8	1 GLUR_HUMAN	P02729 homo sapien
13	2	20.0	8	1 LCK4_LEUMA	P21143 leucophaea
14	2	20.0	8	1 LCK5_LEUMA	P19987 leucophaea
15	2	20.0	8	1 ORMY_ORCLI	P82455 orconectes
16	2	20.0	8	1 PKP3_PERAM	P82618 periplaneta
17	2	20.0	8	1 UC26_MAIZE	P80632 zea mays (m
18	2	20.0	8	1 VGLG_HSV2B	P81780 herpes simp
19	2	20.0	9	1 COXE_THUOB	P80975 thunnus obe
20	2	20.0	9	1 DSIP_RABIT	P01158 oryctolagus
21	2	20.0	9	1 FAR5_ASCSU	P43170 ascaris suu
22	2	20.0	9	1 FARB_CALVO	P41861 calliphora
23	2	20.0	9	1 FIBB_MACFU	P19345 macaca fusc
24	2	20.0	9	1 FIBB_PAPAN	P19344 papio anubi
25	2	20.0	9	1 IPYR_RHOVI	P82982 rhodopsu
26	2	20.0	9	1 MOSP_CLYJA	P19853 clypeaster
27	2	20.0	9	1 MOSH_CLYJA	P19852 clypeaster
28	2	20.0	9	1 NEUJ_CAYPO	P34966 cavia porce
29	2	20.0	9	1 NEUX_HUMAN	P04277 homo sapien
30	2	20.0	9	1 OXYT_OCTVU	P80027 octopus vul
31	2	20.0	9	1 TKLL_LOCHI	P16223 locusta mig
32	2	20.0	9	1 TRP4_LEUMA	P81736 leucophaea
33	2	20.0	9	1 XYLA_STRSQ	P19149 streptomyce

34 2 20.0 10 1 CAER_LITXA P56264 litoria xan
35 2 20.0 10 1 COXO_THUOB P80982 thunnus obe
36 2 20.0 10 1 COXQ_RABIT P80336 oryctolagus
37 2 20.0 10 1 ESTA_SCHGA P81012 schizaphis
38 2 20.0 10 1 FARP_MYTED P42560 mytilus edu
39 2 20.0 10 1 FIBB_CERSI P14537 ceratotheri
40 2 20.0 10 1 GAJU_HUMAN P01358 homo sapien
41 2 20.0 10 1 GLEM_HUMAN P02728 petromyzon
42 2 20.0 10 1 GON3_PETMA P30948 petromyzon
43 2 20.0 10 1 HTF_HELZE P16353 heliothis z
44 2 20.0 10 1 MALE_KLEPN Q05564 kleisiella
45 2 20.0 10 1 MOSQ_CLYJA P19962 clypeaster

ALIGNMENTS

RESULT 1
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 2.1.
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
RC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EF 5
Db 2 EF 3

RESULT 2
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996)
 CC -|- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 ACTIVITY.

CC -|- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -|- MASS SPECTROMETRY: MW=655; METHOD=FAB.

KW Amphibian skin; Amidation.

FT MOD_RES 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EF 5

DB 2 EF 3

RESULT 3

UXA4_CHLTR

ID UXA4_CHLTR STANDARD; PRT; 5 AA.

AC P38005;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Unknown protein from 2D-page from elementary body (Fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE.

RC STRAIN=L2/434/Bu;

RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

RA Comanducci M., Christianen G., Birkelund S., Viretou E., Ratti G.,

RA Pallini V.;

RA Submitted (SEP-1994) to the SWISS-PROT data bank.

CC -|- MISCELLANEOUS; ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

PROTEIN IS: 4.5 ITS MW IS: 28 kDa.

DR Slena-ZDPAGE; P38005; -.

FT NON_TER 5

SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10

DB 2 SG 3

RESULT 4

FARP_MONEX

ID FARP_MONEX STANDARD; PRT; 6 AA.

AC P41966;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FMRamide-like neuropeptide GNFRF-amide.

OS Moniezia expansa (Sheep tapeworm).

OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;

OC Cyclophyllidae; Anoplocephalidae; Moniezia.

OX NCBI_TaxID=28841;

RN [1]

RP SEQUENCE.

RC MEDLINE=93312289; PubMed=8323531;

RA Maule A.G., Shaw C., Halton D.W., Thim L.;

RA "GNFRFamide: a novel FMRamide-immunoreactive peptide isolated from

the sheep tapeworm, Moniezia expansa.";

RT Blochem. Biophys. Res. Commun. 193:1054-1060(1993).

RL

CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 6 AA; 787 MW; 69D409C9C4481000 CRC64;

SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FR 6

DB 4 FR 5

RESULT 5

TRPI_PSEPU

ID TRPI_PSEPU STANDARD; PRT; 6 AA.

AC P36414;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE TrpBA operon transcriptional activator (Fragment).

GN TRPI.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PPG1 C15;

RX MEDLINE=89335826; PubMed=2503057;

RA Eberly L., Crawford I.P.;

RT "DNA sequence of the tryptophan synthase genes of pseudomonas

putida";

RL Biochimie 71:521-531(1989).

CC -|- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE

TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

CC -|- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

REGULATORS.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X13299; CAA31660.1; -.

DR InterPro; IPR000847; HTH_LYSR.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.

KW Tryptophan biosynthesis; Transcription regulation; Activator;

KW DNA-binding.

FT NON_TER 6

SQ SEQUENCE 6 AA; 683 MW; 77672AA1DD6F000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 HD 8

DB 3 HD 4

RESULT 6

UN06_CLOPA

ID UN06_CLOPA STANDARD; PRT; 6 AA.

AC P81351;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 KDa.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
 ||
 Db 4 AE 5

RESULT 7
 ID FARL_ASCSU STANDARD; PRT; 7 AA.
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRPamide-like neuropeptide Af1.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "Af1, a sequenced bioactive neuropeptide isolated from the nematode
 RT Ascaris suum."
 RL Neuron 2:1465-1473(1989).
 CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTONEURONS. REDUCES THE
 CC INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CC CELLS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EF 5
 ||
 Db 3 EF 4

RESULT 8
 ID UF03_MOUSE STANDARD; PRT; 7 AA.
 AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DBDB1B1180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
 ||
 Db 4 AE 5

RESULT 9
 ID AL17_CARMA STANDARD; PRT; 8 AA.
 AC P81820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 17.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
 ||
 Db 1 SG 2

RESULT 10
 ID CCKN_MACEU STANDARD; PRT; 8 AA.
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

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DE Cholecystokinin (CKK).
GN CKK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
CC PIR: A43001; A43001.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MD 2
Db 6 MD 7

RESULT 11
CPDL_ENTFA
ID CPDL_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPDL.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPDL IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOGIN PLASMID PPDL.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 865B729C682C729 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SG 10
Db 7 SG 8

RESULT 12
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem J. 123:25p-25p(1971).
CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR; A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GAL. . .).
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1EB1E CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 HD 8
Db 5 HD 6

RESULT 13
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoides; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DA 3
Db 1 DA 2

RESULT 14
LCK5_LEUMA
ID LCK5_LEUMA STANDARD; PRT; 8 AA.

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Search completed: April 21, 2003, 12:10:27
Job time : 8.33333 secs

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AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
RW Neuropeptide: Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SG 10
Db 2 SG 3

RESULT 15
ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomyotropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Astacidea; Astacoidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdick S., Sauter A., Keller R.;
RT "Two orconekins and the novel octapeptide orcomyotropin in the hindgut
RT of the crayfish Orconectes limosus: identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion.";
RL J. Exp. Biol. 203:2807-2818(2000).
CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
CC BY ABDOMINAL GANGLIONIC NEURONS.
CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DA 3
Db 2 DA 3

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:10 ; Search time 11.6667 Seconds
(without alignments)
82.401 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAEFRHDSG 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	5	A26830	mitosis inhibiting
2	3	30.0	7	PT0283	Ig heavy chain CRD
3	3	30.0	8	S78036	ribosomal protein
4	3	30.0	9	PL0139	carbon-monoxide de
5	3	30.0	10	PH0900	T-cell receptor be
6	2	20.0	3	PT0571	T-cell receptor be
7	2	20.0	4	151049	metallothionein-A
8	2	20.0	4	PT0633	T-cell receptor be
9	2	20.0	4	PT0711	T-cell receptor be
10	2	20.0	4	PT0698	T-cell receptor be
11	2	20.0	4	PT0677	T-cell receptor be
12	2	20.0	4	PT0706	T-cell receptor be
13	2	20.0	4	PT0675	T-cell receptor be
14	2	20.0	4	PT0566	T-cell receptor be
15	2	20.0	5	A32516	cholecystokinin-5
16	2	20.0	5	C23751	spinal cord peptid
17	2	20.0	5	A41225	copper resistance
18	2	20.0	5	B41225	copper resistance
19	2	20.0	5	B31836	20k protein - Rick
20	2	20.0	5	D60274	major protein anti
21	2	20.0	5	D37988	acid proteinase li
22	2	20.0	5	A44692	fulicin - giant Af
23	2	20.0	5	JT0520	Ig kappa chain V-I
24	2	20.0	5	D44823	synaptosomal-assoc
25	2	20.0	5	PT0596	T-cell receptor be
26	2	20.0	5	PT0513	T-cell receptor be
27	2	20.0	5	PT0600	T-cell receptor be
28	2	20.0	5	PT0608	T-cell receptor be
29	2	20.0	5	PT0669	T-cell receptor be

30 2 20.0 5 2 PT0553 T-cell receptor be
31 2 20.0 5 2 PT0538 T-cell receptor be
32 2 20.0 5 2 PT0540 T-cell receptor be
33 2 20.0 5 2 PT0703 T-cell receptor be
34 2 20.0 5 2 PT0690 T-cell receptor be
35 2 20.0 5 2 PT0707 T-cell receptor be
36 2 20.0 5 2 PT0573 T-cell receptor be
37 2 20.0 5 2 PT0572 T-cell receptor be
38 2 20.0 5 2 PT0679 T-cell receptor be
39 2 20.0 5 2 PT0701 T-cell receptor be
40 2 20.0 5 2 PT0717 T-cell receptor be
41 2 20.0 6 2 S02617 alcohol dehydrogen
42 2 20.0 6 2 JU0355 lipopeptide WS1279
43 2 20.0 6 2 S29637 jacalin beta-II ch
44 2 20.0 6 2 A60494 antineoplastic gly
45 2 20.0 6 2 I51434 H4 histone - Afric

ALIGNMENTS

RESULT 1

A26830
mitosis inhibiting peptide - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A26830
R:Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A:Reference number: A26830; MUID:87298602; PMID:3619940
A:Accession: A26830
A:Molecule type: protein
A:Residues: 1-5 <REI>
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DSG 10

DB 3 DSG 5

RESULT 2

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAE 4

DB 1 DAE 3

RESULT 3

S78036	ribosomal protein Yms-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)	
	C:Species: Saccharomyces cerevisiae	
R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma	C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997	
	C:Accession: S78036	
Eur. J. Biochem. 245, 449-456, 1997	A:Title: Identification and characterization of the genes for mitochondrial ribosomal pr	
	A:Reference number: S78018; MUID:97296414; PMID:9151978	
A:Accession: S78036	A:Molecule type: protein	
	A:Residues: 1-8 <KIT>	
C:Keywords: mitochondrion; protein biosynthesis; ribosome	Query Match 30.0%; Score 3; DB 2; Length 8;	
	Best Local Similarity 100.0%; Pred. No. 2.8e+05;	
QY	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	Db 6 DSG 8	
PL0139	carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr	
	C:Species: Pseudomonas carboxydoflava	
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.	C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993	
	C:Accession: PL0139	
Arch. Microbiol. 152, 335-341, 1989	A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotro	
	A:Reference number: PL0138; MUID:90055678; PMID:2818128	
A:Accession: PL0139	A:Molecule type: protein	
	A:Residues: 1-9 <KRA>	
A:Note: 2-Met is also found	C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me	
	C:Keywords: oxidoreductase	
QY	Query Match 30.0%; Score 3; DB 2; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 2.8e+05;	
Db	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	2 DAE 4	
PH0900	T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)	
	C:Species: Rattus norvegicus (Norway rat)	
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.	C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997	
	C:Accession: PH0900	
J. Exp. Med. 174, 1467-1476, 1991	A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg	
	A:Reference number: PH0891; MUID:92078857; PMID:1836012	
A:Accession: PH0900	A:Molecule type: mRNA	
	A:Residues: 1-10 <GOL>	
C:Keywords: T-cell receptor	Query Match 30.0%; Score 3; DB 2; Length 10;	
	Best Local Similarity 100.0%; Pred. No. 1.3e+03;	
QY	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	8 DSG 10	
Db	5 DSG 7	
PT0571	T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)	
	C:Species: Mus musculus (house mouse)	
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001	C:Accession: PT0571	
	R:Feeney, A.J.	
J. Exp. Med. 174, 115-124, 1991	A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions	
	A:Reference number: PT0509; MUID:91277601; PMID:1711558	
A:Accession: PT0571	A:Molecule type: mRNA	
	A:Residues: 1-3 <FEE>	
A:Experimental source: day 19 fetal thymus, strain BALB/c	Query Match 20.0%; Score 2; DB 3; Length 3;	
	Best Local Similarity 100.0%; Pred. No. 2.8e+05;	
C:Keywords: T-cell receptor	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	9 SG 10	
DB	2 SG 3	
IS1049	metallothionein-A - rainbow trout (fragment)	
	C:Species: Oncorhynchus mykiss (rainbow trout)	
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000	C:Accession: IS1049	
	R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.	
Eur. J. Biochem. 230, 344-349, 1995	A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)	
	A:Reference number: IS1049; MUID:95324545; PMID:7601121	
A:Accession: IS1049	A:Status: preliminary; translated from GB/EMBL/DBJ	
	A:Molecule type: DNA	
A:Residues: 1-4 <OLS>	Query Match 20.0%; Score 2; DB 2; Length 4;	
	Best Local Similarity 100.0%; Pred. No. 2.8e+05;	
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	1 MD 2	
QY	1 MD 2	
	Db 1 MD 2	
PT0633	T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)	
	C:Species: Mus musculus (house mouse)	
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997	C:Accession: PT0633	
	R:Feeney, A.J.	
J. Exp. Med. 174, 115-124, 1991	A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions	
	A:Reference number: PT0509; MUID:91277601; PMID:1711558	
A:Accession: PT0633	A:Molecule type: mRNA	
	A:Residues: 1-4 <FEE>	
A:Experimental source: newborn thymus, strain BALB/c	Query Match 20.0%; Score 2; DB 2; Length 4;	
	Best Local Similarity 100.0%; Pred. No. 2.8e+05;	
C:Keywords: T-cell receptor	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	8 DSG 10	
Db	5 DSG 7	

QY 9 SG 10
||
Db 2 SG 3

RESULT 9

T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0607
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE1>
A:Experimental source: newborn thymus, strain BALB/c, 120-2J
A:Accession: PT0674
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A:Accession: PT0570
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE4>
A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A:Accession: PT0711
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE5>
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
||
Db 2 SG 3

RESULT 10

PT0698
T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C:Accession: PT0546; PT0698; PT0583
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0546
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH
A:Accession: PT0698
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, 135-1BP
A:Accession: PT0583
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-4 <FE3>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
||
Db 3 SG 4

RESULT 11

PT0677
T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0558; PT0677
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0558
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG
A:Accession: PT0677
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
||
Db 2 SG 3

RESULT 12

PT0706
T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0706
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0706
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
||
Db 2 SG 3

RESULT 13

PT0675

T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0675
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0675
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FEE>
 A:Experimental source: day 18 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
 ||
 Db 2 SG 3

RESULT 14

PT0566
 T-cell receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0566
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0566
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10
 ||
 Db 2 SG 3

RESULT 15

A32516
 cholecystokinin-5 - dog
 N:Alternate names: CCK-5
 C:Species: Canis lupus familiaris (dog)
 C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C:Accession: A32516
 R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
 Am. J. Physiol. 252, G272-G275, 1987
 A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestine.
 A:Reference number: A32516; MUID:87153871; PMID:3826354
 A:Accession: A32516
 A:Molecule type: protein
 A:Residues: 1-5 <SHI>
 C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin.
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; neuropeptide
 F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MD 2
 ||
 Db 3 MD 4

Search completed: April 21, 2003, 12:12:21
 Job time : 13.6667 secs

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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:12:26 ; Search time 28 Seconds
(without alignments)
73.588 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 5
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mhc.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1	10.0	5	2 P83073	P83073 bacillus ce
2	1	10.0	5	10 Q99007	Q99007 hordeum vul
3	1	10.0	5	13 P83308	P83308 gallus gall
4	1	10.0	6	10 P82181	P82181 spinacia ol
5	1	10.0	6	10 P82541	P82541 spinacia ol
6	1	10.0	6	10 P82182	P82182 spinacia ol

ALIGNMENTS

RESULT 1
P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073
DT 01-OCT-2001 (Tremblrel. 18, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 10.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 M 4
|
Db 1 M 1

RESULT 2
Q99007
ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (fragment).
GN Amyl.

OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers.";
RT Plant Mol. Biol. 16:713-721(1991).

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
CC EMBL; X54643; CAA38455.1; -;
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5

SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 10.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 M 4
|
Db 1 M 1

RESULT 3
P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE FMRamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-BRAIN;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 ET antibodies to FMRamide";
 RL Nature 305:328-330(1983).
 CC -|- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -|- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 10.0%; Score 1; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 R 9
 DB 4 R 4

RESULT 4
 P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Magnoliophytales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -|- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal_L10.
 DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 DR Pfan; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DE8000 CRC64;

Query Match 10.0%; Score 1; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 A 6
 DB 1 A 1

RESULT 5
 P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28465-28465(2000).
 CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -|- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -|- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -|- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR Pfan; PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 10.0%; Score 1; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 R 9
 DB 2 R 2

RESULT 6
 P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.

CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF0466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 10.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 A 6
Db 1 A 1

Search completed: April 21, 2003, 12:15:07
Job time : 28 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:11:46 ; Search time 10 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 5

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2	20.0	5	RE21_LITRU	P82071 litoria rub
2	2	20.0	5	RE31_LITRU	P82072 litoria rub
3	2	20.0	5	UC22_MAIZE	P80628 zea mays (m
4	2	20.0	6	FARP_MONEX	P41966 moniezia ex
5	2	20.0	6	UN06_CLOPA	P81351 clostridium
6	1	10.0	5	AL14_CARMA	P81817 carcinus ma
7	1	10.0	5	BIOA_CITFR	P13071 citrobacter
8	1	10.0	5	BIOE_CITFR	P12997 citrobacter
9	1	10.0	5	BPP7_BOTIN	P30425 bothrops in
10	1	10.0	5	EI03_LITRU	P82099 litoria rub
11	1	10.0	5	EI04_LITRU	P82100 litoria rub
12	1	10.0	5	FARP_ARTTR	P41853 artiposthi
13	1	10.0	5	PAP2_PARMA	P81864 pardachirus
14	1	10.0	5	PRCT_PPRAM	P01373 periplaneta
15	1	10.0	5	RE11_LITRU	P82070 litoria rub
16	1	10.0	5	RE32_LITRU	P82073 litoria rub
17	1	10.0	5	SUGA_ACHDO	P19991 acheta dome
18	1	10.0	5	TPIS_CANFA	P54714 canis famil
19	1	10.0	5	TRM3_ECOLI	P13973 escherichia
20	1	10.0	5	UF01_MOUSE	P38639 mus musculus
21	1	10.0	5	UXA4_CHLTR	P38005 chlamydia t
22	1	10.0	6	ACPH_RABIT	P25154 oryctolagus
23	1	10.0	6	ASP2_LACSN	P82655 lactobacill
24	1	10.0	6	CIP1_MYTED	P13736 mytilus edu
25	1	10.0	6	CIP2_MYTED	P13737 mytilus edu
26	1	10.0	6	EI01_LITRU	P82096 litoria rub
27	1	10.0	6	LOK1_LOCMI	P41491 locusta mig
28	1	10.0	6	OVW_LEPDE	P42985 leptonotars
29	1	10.0	6	TMOF_SARBU	P41495 sarcophaga
30	1	10.0	6	TRPI_PSEPU	P36414 pseudomonas
31	1	10.0	6	VP19_HSV1K	P23210 herpes simp
32	0	0.0	5	PSK_DAUCA	P58261 daucus caro

ALIGNMENTS

```
RESULT 1
RE21_LITRU          STANDARD;          PRT;          5 AA.
ID   P82071;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodyadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australian red tree frog
RT   'Litoria rubella', the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC   ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;
      Query Match      20.0%; Score 2; DB 1; Length 5;
      Best Local Similarity 100.0%; Pred. No. 1.le+05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   7 EF 8
DB   2 EF 3

RESULT 2
RE31_LITRU          STANDARD;          PRT;          5 AA.
ID   P82072;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodyadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australian red tree frog
RT   'Litoria rubella', the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC   ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES 5
SQ   SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
      Query Match      20.0%; Score 2; DB 1; Length 5;
```

Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EF 8
Db 2 EF 3

RESULT 3

UC22_MAIZE UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR Maize-2DPAGE: P80628; COLEOPTILE.
DR MaizeDB: 123954; .
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C0C300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EV 2
Db 4 EV 5

RESULT 4

FARP_MONEX FARP_MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRamide-like neuropeptide GNFRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa."
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
FT SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FR 9
Db 4 FR 5

RESULT 5

UN06_CLOPA UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
FT NON_TER 6 6
FT SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AE 7
Db 4 AE 5

RESULT 6

ALI4_CARMA ALI4_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5
FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      8 F 8
Db      3 F 3

RESULT 7
BIOB_CITR
ID      BIOB_CITR      STANDARD;      PRT;      5 AA.
AC      P13071;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE      (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE      aminotransferase) (Fragment).
GN      BIOA.
OS      Citrobacter freundii.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Citrobacter.
OX      NCBI_TaxID=546;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89006280; PubMed=2971595;
RA      Shiuan D., Campbell A.;
RT      "Transcriptional regulation and gene arrangement of Escherichia coli,
RT      Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL      Gene 67:203-211(1988).
CC      -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC      oxononanoate -> S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC      diaminononanoate.
CC      -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -!- PATHWAY: Biotin biosynthesis.
CC      -!- SUBUNIT: HOMODIMER.
CC      -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC      AMINOTRANSFERASES.
-----
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-----
EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR      InterPro; IPR000954; AminoTran_3
DR      PROSITE; PS006500; AA_TRANSFER_CLASS_3; PARTIAL.
KW      Biotin biosynthesis; Transferase; Aminotransferase;
KW      Pyridoxal phosphate.
FT      NON_TER      5
SQ      SEQUENCE      5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match      10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 M 4
Db      1 M 1

RESULT 8
BIOB_CITR
ID      BIOB_CITR      STANDARD;      PRT;      5 AA.
AC      P12997;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN      BIOB.
OS      Citrobacter freundii.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC      Citrobacter.
OX      NCBI_TaxID=546;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89006280; PubMed=2971595;
RA      Shiuan D., Campbell A.;
RT      "Transcriptional regulation and gene arrangement of Escherichia coli,
RT      Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL      Gene 67:203-211(1988).
CC      -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC      -!- PATHWAY: Biotin biosynthesis; last step.
CC      -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC      FAMILY.
-----
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-----
EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR      Biotin biosynthesis; Iron-sulfur; Transferase.
FT      NON_TER      5
SQ      SEQUENCE      5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match      10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 M 4
Db      1 M 1

RESULT 9
BPP7_BOTIN
ID      BPP7_BOTIN      STANDARD;      PRT;      5 AA.
AC      P30425;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      01-FEB-1994 (Rel. 28, Last annotation update)
DE      Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE      enzyme inhibitor)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodonta; Squamata; Serpentes; Colubroidea;
OC      Viperidae; Crotalinae; Bothrops.
OX      NCBI_TaxID=8723;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=90351557; PubMed=2386615;
RA      Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT      "Primary structure and biological activity of bradykinin potentiating
RT      peptides from Bothrops insularis snake venom.";
RL      J. Protein Chem. 9:221-227(1990).
CC      -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC      ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC      BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC      IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR      PIR; G37196; G37196.
KW      Hypotensive agent; Venom.
FT      MOD_RES      1
SQ      SEQUENCE      5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match      10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 K 3

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Db      2 K 2

RESULT 10
E103_LITRU
ID E103_LITRU STANDARD; PRT; 5 AA.
AC P8209;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 F 8
DB 1 F 1

RESULT 11
E104_LITRU
ID E104_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 F 8
DB 1 F 1

RESULT 12
FARP_ARTTR
ID FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide RYIRF-amide.
OS Artiopesthia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplaneidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 R 9
DB 1 R 1

RESULT 13
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -|- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -|- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 F 8
DB 2 F 2

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RESULT 14
 PRCT_PERAM STANDARD; PRT; 5 AA.
 AC POL373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Proctolin.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 in insects.";
 RL Life Sci. 17:1253-1256(1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron.";
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 horseshoe crab, Limulus polyphemus.";
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Stangier J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 R 9
 |
 DB 1 R 1

RESULT 15
 RE11_LITRU STANDARD; PRT; 5 AA.
 ID RE11_LITRU
 AC PR2070;
 DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella'. the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=598; METHOD=Fab.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 10.0%; Score 1; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 V 2
 |
 DB 1 V 1

Search completed: April 21, 2003, 12:14:33
 Job time : 10 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:13:41 ; Search time 14 seconds
(without alignments)
68.667 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 230

Minimum DB seq length: 5
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2	20.0	5	2 A32516	cholecystokinin-5
2	2	20.0	5	2 C23751	spinal cord peptid
3	2	20.0	5	2 B41225	copper resistance
4	2	20.0	5	2 B31836	20K protein - Rick
5	2	20.0	5	2 P00009	angiotensin-conver
6	2	20.0	5	2 B37988	acid proteinase li
7	2	20.0	5	2 A44692	fulicin - giant Af
8	2	20.0	5	2 P00596	T-cell receptor be
9	2	20.0	5	2 P00538	T-cell receptor be
10	2	20.0	6	2 S02617	alcohol dehydrogen
11	2	20.0	6	2 S11024	hydrogensulfite re
12	2	20.0	6	2 A20186	fatty-acid synthas
13	2	20.0	6	2 A46474	FC epsilon Riib -
14	2	20.0	6	2 P00616	T-cell receptor be
15	2	20.0	6	2 P00687	T-cell receptor be
16	2	20.0	6	2 P00650	T-cell receptor be
17	2	20.0	6	2 P00550	T-cell receptor be
18	2	20.0	6	2 P00587	T-cell receptor be
19	2	20.0	6	2 P00568	T-cell receptor be
20	2	20.0	6	2 P00693	T-cell receptor be
21	2	20.0	6	2 A43129	neuropeptide GNFRR
22	1	10.0	5	1 HOROHA	proctolin - Americ
23	1	10.0	5	2 A60521	glycogen phosphory
24	1	10.0	5	2 JN0862	peptidyl-dipectida
25	1	10.0	5	2 JN0860	peptidyl-dipectida
26	1	10.0	5	2 A26830	mitosis inhibiting
27	1	10.0	5	2 C41225	copper resistance
28	1	10.0	5	2 A41225	copper resistance
29	1	10.0	5	2 S70154	URF2 protein - Xan

30	1	10.0	5	2 I40702	primase - Citrobac
31	1	10.0	5	2 I40698	biotin B - Citroba
32	1	10.0	5	2 B37325	pap fibmbrial regul
33	1	10.0	5	2 A32014	tram protein - Esc
34	1	10.0	5	2 E42364	flagellar protein
35	1	10.0	5	2 A44955	alkanal monooxygen
36	1	10.0	5	2 I39984	ribosomal protein
37	1	10.0	5	2 I39966	ribosomal protein
38	1	10.0	5	2 I39965	ribosomal protein
39	1	10.0	5	2 I40469	dnazX-like protein
40	1	10.0	5	2 B60274	major protein anti
41	1	10.0	5	2 D60274	major protein anti
42	1	10.0	5	2 S60274	endo-1,4-beta-xyla
43	1	10.0	5	2 S70615	R-phycoerythrin al
44	1	10.0	5	2 B22565	R-phycoerythrin al
45	1	10.0	5	2 F22565	R-phycoerythrin ga

ALIGNMENTS

RESULT 1
A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, A.M. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and i
A:Reference number: A32516; MUID:87153871; PMID:3826354
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SH1>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholec
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5
Db 3 MD 4

RESULT 2
C23751
spinal cord peptide SCP-6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C:Accession: C23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tso
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: C23751
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <HS1>
C:Superfamily: unassigned animal peptides

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DA 6
Db 1 DA 2

RESULT 3

B41225
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: B41225
R:Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane proteins
A:Reference number: A41225; MUID:92020961; PMID:1924351
A:Accession: B41225
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AE 7
||
Db 1 AE 2

RESULT 4

B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A:Reference number: A91885; MUID:89008059; PMID:3139629
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 1-5 <AND>
A:Cross-references: GB:J03371; NID:gl52455; PIDN:AAD15030.1; PID:g4262874

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MD 5
||
Db 1 MD 2

RESULT 5

PQ0009
angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N:Alternate names: ficus latex peptide 2
C:Species: Ficus carica (common fig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C:Accession: PQ0009
R:Wariyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0009
A:Molecule type: protein
A:Residues: 1-5 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
||
Db 4 VK 5

RESULT 6

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum
A:Reference number: A37988; MUID:91060608; PMID:2246266
A:Accession: B37988
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AE 7
||
Db 1 AE 2

RESULT 7

A44692
fulicin - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C:Accession: A44692
R:Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; Blochem. Biophys. Res. Commun. 178, 486-493, 1991
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from Achatina fulica
A:Reference number: A44692; MUID:91315471; PMID:1859408
A:Accession: A44692
A:Molecule type: protein
A:Residues: 1-5 <OHT>
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F:2/Modified site: D-asparagine (Asn) #status experimental
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EF 8
||
Db 3 EF 4

RESULT 8

PT0596
T-cell receptor beta chain V-D-J region (100-2AE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0596; PT0614
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0596
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AE
A:Accession: PT0614
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1H
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DA 6
 ||
 DB 4 DA 5

RESULT 9

PT0538
 T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0538; PT0539; PT0603
 J. Feeney, A.J.
 R. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0538
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <PPE>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
 A:Accession: PT0539
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <PE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
 A:Accession: PT0603
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DA 6
 ||
 DB 4 DA 5

RESULT 10

S02617
 alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
 C:Species: Equus caballus (domestic horse)
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
 C:Accession: S02617
 R. Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pates, X.; Vallee, B.L.; Joernvall
 FEBS Lett. 222, 99-103, 1987
 A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differences
 A:Reference number: S02617; MUID:88005160; PMID:3653405
 A:Accession: S02617
 A:Molecule type: protein
 A:Residues: 1-6 <FAI>
 A:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AE 7
 ||
 DB 2 AE 3

RESULT 11

S11024
 hydrogensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)

N:Alternate names: bisulfite reductase; desulfofusicidin
 C:Species: Desulfovibrio thermophilus
 C>Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: S11024
 R. Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G
 Biochim. Biophys. Acta 1040, 112-118, 1990
 A:Title: Purification and characterization of bisulfite reductase (desulfofusicidin)
 A:Reference number: S11024; MUID:90335276; PMID:2165817
 A:Accession: S11024
 A:Molecule type: protein
 A:Residues: 1-6 <FAU>
 C:Keywords: oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
 ||
 DB 3 VK 4

RESULT 12

A20186
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-May-2000
 C:Accession: A20186
 R. McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.
 FEBS Lett. 160, 296-300, 1983
 A:Title: Amino acid sequence around the active serine in the acyl transferase domain
 A:Reference number: A20186; MUID:83287768; PMID:6554204
 A:Accession: A20186
 A:Molecule type: protein
 A:Residues: 1-6 <MCC>
 C:Keywords: acyltransferase; coenzyme A

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EV 2
 ||
 DB 4 EV 5

RESULT 13

A46474
 Fc epsilon RIIB - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
 C:Accession: A46474
 R. Richards, M.L.; Katz, D.H.; Liu, F.T.
 J. Immunol. 147, 1067-1074, 1991
 A:Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Dr
 A:Reference number: A46474; MUID:91318149; PMID:1861070
 A:Accession: A46474
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-6 <RIC>
 A:Experimental source: BALB C, splenic B cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MD 5
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 DB 1 MD 2

RESULT 14

PT0616
T-cell receptor beta chain V-D-J region (120-1G) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0616
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0616
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DA 6
||
Db 4 DA 5

RESULT 15
PT0687
T-cell receptor beta chain V-D-J region (120-2CM) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C:Accession: PT0609; PT0687; PT0541
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0609
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-2CM
A:Accession: PT0687
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1A
A:Accession: PT0541
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c (clone A3/IIC7)
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DA 6
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Db 4 DA 5

Search completed: April 21, 2003, 12:15:50
Job time : 15 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:14:21 ; Search time 15 Seconds
(without alignments)
50.409 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OIIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5763

Minimum DB seq length: 5

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	50.0	5	10	US-09-794-927-72
2	5	50.0	5	10	US-09-795-847-72
3	5	50.0	5	10	US-09-794-743-72
4	5	50.0	5	10	US-09-794-748-72
5	5	50.0	5	10	US-09-794-925-72
6	5	50.0	5	10	US-09-681-442-72
7	4	40.0	6	10	US-09-808-037-7
8	3	30.0	5	9	US-10-179-046-15
9	3	30.0	5	10	US-09-071-838-209
10	3	30.0	6	9	US-09-727-963A-21
11	3	30.0	6	9	US-09-727-963A-87
12	3	30.0	6	9	US-10-059-749-72
13	3	30.0	6	9	US-10-247-488-8
14	3	30.0	6	9	US-10-091-135-89
15	3	30.0	6	10	US-09-765-086-230
16	3	30.0	6	10	US-09-952-768-57
17	3	30.0	6	10	US-09-954-697-110
18	3	30.0	6	10	US-09-982-172-44
19	2	20.0	5	8	US-08-859-699-20

20	2	20.0	5	8	US-08-484-409-23	Sequence 23, Appl
21	2	20.0	5	8	US-08-484-409-38	Sequence 38, Appl
22	2	20.0	5	8	US-08-424-550B-509	Sequence 509, App
23	2	20.0	5	8	US-08-424-550B-716	Sequence 716, App
24	2	20.0	5	9	US-10-020-436A-6	Sequence 6, Appli
25	2	20.0	5	9	US-10-020-436A-11	Sequence 11, Appl
26	2	20.0	5	9	US-10-020-436A-17	Sequence 17, Appl
27	2	20.0	5	9	US-09-976-736-44	Sequence 44, Appl
28	2	20.0	5	9	US-10-000-273-9	Sequence 9, Appli
29	2	20.0	5	9	US-10-091-442-7	Sequence 7, Appli
30	2	20.0	5	9	US-10-100-952-198	Sequence 198, App
31	2	20.0	5	9	US-09-769-145-14	Sequence 14, Appl
32	2	20.0	5	9	US-09-769-145-15	Sequence 15, Appl
33	2	20.0	5	9	US-10-007-363-18	Sequence 18, Appl
34	2	20.0	5	9	US-10-014-485A-78	Sequence 78, Appl
35	2	20.0	5	9	US-10-014-485A-117	Sequence 117, App
36	2	20.0	5	9	US-10-014-485A-118	Sequence 118, App
37	2	20.0	5	9	US-10-014-485A-119	Sequence 119, App
38	2	20.0	5	9	US-10-006-557-9	Sequence 9, Appli
39	2	20.0	5	9	US-10-035-349-13	Sequence 13, Appl
40	2	20.0	5	9	US-09-813-718-56	Sequence 56, Appl
41	2	20.0	5	9	US-10-059-749-20	Sequence 20, Appl
42	2	20.0	5	9	US-10-059-749-21	Sequence 21, Appl
43	2	20.0	5	9	US-10-059-749-31	Sequence 31, Appl
44	2	20.0	5	9	US-10-059-749-42	Sequence 42, Appl
45	2	20.0	5	9	US-10-059-749-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Biquang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794, 927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DAEFR 9
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Db 1 DAEFR 5

RESULT 2

US-09-795-847-72
; Sequence 72, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DAEFR 9

Db 1 DAEFR 5

RESULT 3

US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DAEFR 9

Db 1 DAEFR 5

RESULT 4

US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DAEFR 9

Db 1 DAEFR 5

RESULT 5

US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.

;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Chung, Ling-Fong
;; REGISTRATION NUMBER: 36,482
;; REFERENCE/DOCKET NUMBER: 1165.100
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 601-2704
;; TELEFAX: (510) 655-3542
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-179-046-15

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EFR 9
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DB 3 EFR 5

RESULT 9

US-09-071-838-209
; Sequence 209, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:

; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-0861000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-071-838-209

Query Match 30.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KMD 5
|||
DB 1 KMD 3

RESULT 10

US-09-727-963A-21
; Sequence 21, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-21

Query Match 30.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FRH 10
|||
DB 4 FRH 6

RESULT 11

US-09-727-963A-87
; Sequence 87, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: wherein Xaa is D-phenylalanine
US-09-727-963A-87

Query Match 30.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVK 3

Db III
 3 EVK 5

RESULT 12

US-10-059-749-72
; Sequence 72, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-059-749-72

Query Match 30.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 7 EFR 9
 III
Db 1 EFR 3

RESULT 13

US-10-247-488-8
; Sequence 8, Application US/10247488
; Publication No. US2003002244A1
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336-RAMOT
; CURRENT APPLICATION NUMBER: US/10/247,488
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/526,738
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Humanus
US-10-247-488-8

Query Match 30.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 FRH 10
 III
Db 1 FRH 3

RESULT 14

US-10-091-135-89
; Sequence 89, Application US/10091135
; Publication No. US2003003960A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-091-135-89

Query Match 30.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 6 AEF 8
 III
Db 4 AEF 6

RESULT 15

US-09-765-086-230
; Sequence 230, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.
; APPLICANT: Ellierby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-09-765-086-230

Query Match 30.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVK 3
Db 2 EVK 4

Search completed: April 21, 2003, 12:16:10
Job time : 15 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:13:01 ; Search time 14 Seconds
(without alignments)

21.016 Million cell updates/sec

Title: US-09-580-018-5

Perfect score: 10

Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 23591

Minimum DB seq length: 5

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	50.0	5	1 US-08-480-498-1	Sequence 1, Appli
2	5	50.0	5	2 US-08-422-333-7	Sequence 7, Appli
3	5	50.0	5	2 US-08-659-984A-13	Sequence 13, Appli
4	5	50.0	5	4 US-08-660-531-13	Sequence 13, Appli
5	5	50.0	5	4 US-09-054-334-1	Sequence 1, Appli
6	5	50.0	5	5 5187153-6	Patent No. 5187153
7	5	50.0	5	5 5220013-6	Patent No. 5220013
8	5	50.0	5	6 5223482-6	Patent No. 5223482
9	4	40.0	6	1 US-07-965-971-3	Sequence 3, Appli
10	4	40.0	6	1 US-08-143-697-3	Sequence 3, Appli
11	4	40.0	6	1 US-08-440-261-3	Sequence 3, Appli
12	4	40.0	6	1 US-08-440-423-3	Sequence 3, Appli
13	4	40.0	6	2 US-08-025-321C-2	Sequence 2, Appli
14	4	40.0	6	3 US-08-846-444-3	Sequence 3, Appli
15	3	30.0	5	1 US-08-297-330-11	Sequence 11, Appli
16	3	30.0	5	2 US-08-719-758-16	Sequence 16, Appli
17	3	30.0	5	2 US-08-637-759B-303	Sequence 303, App
18	3	30.0	5	3 US-08-871-355A-303	Sequence 303, App
19	3	30.0	5	3 US-09-029-267-15	Sequence 15, Appl
20	3	30.0	5	4 US-09-119-827-16	Sequence 16, Appl
21	3	30.0	5	4 US-09-177-249-209	Sequence 209, App
22	3	30.0	5	4 US-09-001-984C-24	Sequence 24, Appli
23	3	30.0	5	4 US-09-117-121-9	Sequence 9, Appli
24	3	30.0	5	4 US-09-201-945-303	Sequence 303, App
25	3	30.0	5	4 US-09-187-859-116	Sequence 116, App
26	3	30.0	5	4 US-09-187-859-117	Sequence 117, App
27	3	30.0	5	4 US-09-187-859-119	Sequence 119, App

28 3 30.0 5 4 US-09-187-859-910 Sequence 910, App
29 3 30.0 5 4 US-09-187-859-925 Sequence 925, App
30 3 30.0 5 4 US-09-187-859-930 Sequence 930, App
31 3 30.0 5 4 US-09-187-859-935 Sequence 935, App
32 3 30.0 5 4 US-09-187-859-950 Sequence 950, App
33 3 30.0 5 4 US-09-187-859-951 Sequence 951, App
34 3 30.0 5 4 US-09-187-859-952 Sequence 952, App
35 3 30.0 5 4 US-09-187-859-953 Sequence 953, App
36 3 30.0 5 4 US-09-187-859-955 Sequence 955, App
37 3 30.0 5 4 US-09-187-859-956 Sequence 956, App
38 3 30.0 5 4 US-09-187-859-970 Sequence 970, App
39 3 30.0 5 4 US-09-187-859-972 Sequence 972, App
40 3 30.0 5 4 US-09-187-859-973 Sequence 973, App
41 3 30.0 5 4 US-08-836-047-4 Sequence 4, Appli
42 3 30.0 5 4 US-09-297-269-14 Sequence 14, Appl
43 3 30.0 5 5 PCT-US93-12679-21 Sequence 21, Appl
44 3 30.0 5 5 PCT-US93-12679-37 Sequence 37, Appl
45 3 30.0 5 5 PCT-US94-02391-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-480-498-1
; Sequence 1, Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-498-1

Query Match 50.0%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6

Db 1 VKMDA 5

RESULT 2

US-08-422-333-7
; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-7

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8

|||||

DB 1 MDAEF 5

RESULT 3

US-08-659-984A-13
; Sequence 13, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-0028100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-659-984A-13

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6

|||||

DB 1 VKMDA 5

RESULT 4

US-08-660-531-13
; Sequence 13, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-0022100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
US-08-660-531-13

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
Db 1 VKMDA 5

RESULT 5

US-09-054-334-1
; Sequence 1, Application US/09054334
; Patent No. 6329163
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Jacobson-Croak, Kirsten L.
; APPLICANT: Sinha, Sukanto
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,334
; FILING DATE: 02-APR-1998
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 015270-002820US
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-334-1

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
Db 1 VKMDA 5

RESULT 6

5187153-6
; Patent No. 5187153

;/ APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
;/ TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
;/ AMYLOID POLYPEPTIDE DERIVATIVES
;/ NUMBER OF SEQUENCES: 33
;/ CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6;
; LENGTH: 5
5187153-6

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8
Db 1 MDAEF 5

RESULT 7

5220013-6

;/ Patent No. 5220013
;/ APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
;/ TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
;/ OF ALZHEIMER'S DISEASE

;/ NUMBER OF SEQUENCES: 30
;/ CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987

;/ APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6;
; LENGTH: 5
5220013-6

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8
Db 1 MDAEF 5

RESULT 8

5223482-6

;/ Patent No. 5223482
;/ APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
;/ BARBARA
;/ TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
;/ INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
;/ NUMBER OF SEQUENCES: 34

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/361,912
;; FILING DATE: 06-JUN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 359,911
;; FILING DATE: 12-MAY-1989
;; APPLICATION NUMBER: 87,002
;; FILING DATE: 18-AUG-1987
;; APPLICATION NUMBER: 8,810
;; FILING DATE: 30-JAN-1987
;; APPLICATION NUMBER: 948,376
;; FILING DATE: 31-DEC-1986
;; APPLICATION NUMBER: 932,193
;; FILING DATE: 17-NOV-1986
;; SEQ ID NO: 6:
5223482-6
LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8
Db 1 MDAEF 5

RESULT 9
US-07-965-971-3
; Sequence 3, Application US/07965971
; Patent No. 5441870
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.
; APPLICANT: Schenk, Dale B.
; APPLICANT: Fritz, Lawrence C.
; TITLE OF INVENTION: Methods and Compositions for Monitoring
; TITLE OF INVENTION: Cellular Processing of Beta-Amyloid Precursor Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,971
; FILING DATE: 26-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,949
; FILING DATE: 15-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-4-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-965-971-3

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKM 4
Db 3 EVKM 6
RESULT 10
US-08-143-697-3
; Sequence 3, Application US/08143697
; Patent No. 5604102
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.
; APPLICANT: Schenk, Dale B.
; APPLICANT: Fritz, Lawrence C.
; TITLE OF INVENTION: Methods of Screening for Beta-Amyloid
; TITLE OF INVENTION: Peptide Production Inhibitors
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/143,697
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,971
; FILING DATE: 26-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,949
; FILING DATE: 15-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-4-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-143-697-3

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKM 4
Db 3 EVKM 6

RESULT 11
US-08-440-261-3
; Sequence 3, Application US/08440261
; Patent No. 5605811
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.

```
; APPLICANT: Schenk, Dale B.
; APPLICANT: Fritz, Lawrence C.
; TITLE OF INVENTION: Methods and Compositions for Monitoring
; TITLE OF INVENTION: Cellular Processing of Beta-Amyloid Precursor Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,261
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,971
; FILING DATE: 26-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-4-3
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-440-261-3

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 EVKM 4
Db 3 EVKM 6

RESULT 12
US-08-440-423-3
; Sequence 3, Application US/08440423
; Patent No. 5721130
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Methods and Compositions for Monitoring
; TITLE OF INVENTION: Cellular Processing of Beta-Amyloid Precursor Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 EVKM 4
Db 3 EVKM 6

RESULT 13
US-08-025-321C-2
; Sequence 2, Application US/08025321C
; Patent No. 5849560
; GENERAL INFORMATION:
; APPLICANT: Abraham Ph.D., Carmela R.
; TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGRADATION
; TITLE OF INVENTION: OF AMYLOID BETA-PROTEIN PRECURSOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/025,321C
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0079571-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 248 5000
; TELEFAX: 617 248 4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-025-321C-2

Query Match 40.0%; Score 4; DB 2; Length 6;
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Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4
Db 3 EVKM 6

RESULT 14
US-08-846-444-3
; Sequence 3, Application US/08846444
; Patent No. 6018024
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.
; APPLICANT: Schenk, Dale B.
; APPLICANT: Fritz, Lawrence C.
; TITLE OF INVENTION: Methods and Compositions for Monitoring
; TITLE OF INVENTION: Cellular Processing of Beta-Amyloid Precursor Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,444
; FILING DATE: No. 6018024 yet assigned
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,949
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,971
; FILING DATE: 26-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US93/01817
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,423
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015270-000450US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-846-444-3

Query Match 40.0%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4
Db 3 EVKM 6

US-08-297-330-11
; Sequence 11, Application US/08297330
; Patent No. 5583108
; GENERAL INFORMATION:
; APPLICANT: Wei, Chi-Ming
; APPLICANT: Burnett, John C.
; TITLE OF INVENTION: Vasonatin Peptide and Analogs
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5583108west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,330
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/025,935
; FILING DATE: 03-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 1016.99-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-297-330-11

Query Match 30.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMD 5
Db 1 KMD 3

Search completed: April 21, 2003, 12:15:28
Job time : 14 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:31 ; Search time 34 Seconds
(without alignments)
39.191 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 30890

Minimum DB seq length: 5

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

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23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	60.0	6	19	AAU70868
2	6	60.0	6	23	AAU78525
3	5	50.0	5	14	AAAR37864
4	5	50.0	5	18	AAW08216
5	5	50.0	5	19	AAW61150
6	5	50.0	5	20	AAW33750
7	5	50.0	5	20	AAW08608
8	5	50.0	5	21	RAY69702
9	5	50.0	5	22	AAE10667
10	5	50.0	5	22	AAE06907

11	5	50.0	5	22	AAU06636	Peptide product of
12	5	50.0	5	22	AAU07235	Human beta-amyloid
13	5	50.0	5	22	AAAR7260	Wild type APP sequ
14	5	50.0	5	23	ABO66554	Beta-secretase rel
15	5	50.0	5	23	ABO66579	Amyloid protein pr
16	5	50.0	6	19	AAW70864	Beta-amyloid pepti
17	5	50.0	6	22	AAAR46199	Human APP A-beta 1
18	5	50.0	6	22	AAAR49095	Human amyloid beta
19	4	40.0	6	14	AAAR42400	Peptide representi
20	4	40.0	6	20	AAAR82441	Human amyloid beta
21	4	40.0	6	20	AAAR82441	Epitope #1 used in
22	3	30.0	5	10	AAAR94846	Pentapeptide paral
23	3	30.0	5	12	AAAR12728	Mimotope peptide #
24	3	30.0	5	15	AAAR51592	Peptide signal seq
25	3	30.0	5	15	AAAR59980	Peptide signal seq
26	3	30.0	5	15	AAAR59964	TK-SH2 association
27	3	30.0	5	15	AAAR52938	Natriuretic peptid
28	3	30.0	5	15	AAAR71658	Fulicin-like neuro
29	3	30.0	5	16	AAAR33907	Fulicin-like neuro
30	3	30.0	5	16	AAAR33908	Fulicin-like neuro
31	3	30.0	5	16	AAAR33909	Pentameric mimotop
32	3	30.0	5	16	AAAR69964	Cyclic pentapeptid
33	3	30.0	5	17	AAW09684	Peptide 86 from 88
34	3	30.0	5	17	AAAR98706	P. americanus skin
35	3	30.0	5	18	AAW22867	IDA-peptide capabl
36	3	30.0	5	18	AAW25194	Neuropeptide. Ach
37	3	30.0	5	18	AAW12822	Peptide produced b
38	3	30.0	5	19	AAW70127	Human delta-sarcog
39	3	30.0	5	20	AAW67458	Linker used to fin
40	3	30.0	5	21	AAAY96279	Peptide derived fr
41	3	30.0	5	21	AAAY44441	Cadherin-5 cell ad
42	3	30.0	5	21	AAAY60878	Cadherin-5 cell ad
43	3	30.0	5	21	AAAY60879	Cadherin-5 cell ad
44	3	30.0	5	21	AAAY60881	Cadherin-5 cell ad
45	3	30.0	5	21	AAAY60890	Cadherin-5 cell ad

ALIGNMENTS

RESULT 1
AAW70868
ID AAW70868 standard; peptide; 6 AA.
XX
AC AAW70868;
XX
DT 04-FEB-1999 (first entry)
XX
DE Beta-amyloid peptide to create a monoclonal antibody.
XX
KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
KW antibody; amyloid deposit; Alzheimer's disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9844955-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US06900.
XX
PR 09-APR-1997; 97US-0041850.
XX
(MCIN/) MCINNIS P A.
(MIND-) MINDSET LTD.
PI Chain DG;
XX
XX WPI; 1998-594476/50.
XX
XX Preventing or inhibiting progression of Alzheimer's Disease -
XX comprises use of recombinant DNA encoding an antibody specific for

the N- or C-terminus of an amyloid-beta peptide

Example 1; Page 47; 58pp; English.

The present sequence represents a peptide derived from beta-amyloid precursor protein (beta-APP, see AAU70863). The peptide is a beta-amyloid peptide and is used to produce a monoclonal antibody. The specification describes a method for prevention or inhibition of progression of Alzheimer's disease. The method comprises administering a composition comprising a recombinant DNA molecule containing a gene encoding a recombinant antibody end-specific for the N-terminus or the C-terminus of an amyloid-beta peptide, operably linked to a promoter which is expressed in the central nervous system. The recombinant antibody molecules prevent the accumulation of beta-amyloid peptides in the extracellular space, interstitial fluid and cerebrospinal fluid and the aggregation of such peptides into amyloid deposits in the brain. They also inhibit the progression of Alzheimer's disease by inhibiting the interaction of beta-amyloid peptides mediating Alzheimer's disease induced neurotoxicity and inhibiting the Alzheimer's disease induced complement activation and cytokine release involved in the inflammatory process.

Sequence 6 AA;

Query Match 60.0%; Score 6; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DAEFRH 10
| | | | |
Db 1 DAEFRH 6

RESULT 2

AAU78525
ID AAU78525 standard; Peptide: 6 AA.

AC AAU78525;

DT 18-JUN-2002 (first entry)

DE Beta amyloid precursor protein beta secretase cleavage site.

KW Alzheimer's disease; beta amyloid precursor protein; beta secretase;
KW BACE; beta-site APP cleaving enzyme; nootropic; neuroprotective;
KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
KW BACE secretase/shedase; neurodegenerative disorder.

OS Unidentified.

FH Key Location/Qualifiers

FT Cleavage-site 4..5 /note= "Beta secretase cleavage site"

FX WO200210354-A2.

PN

PD 07-FEB-2002.

PF 01-AUG-2001; 2001WO-CA01118.

PR 01-AUG-2000; 2000CA-2313828.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

PI Seidah NG, Chretien M, Cromlish JA;

XX WPI; 2002-280632/32.

XX Modulating activity of beta-site amyloid precursor protein-cleaving
PT enzyme secretase/shedase for treatment of neurodegenerative disorder
PT characterised by generation of Abeta protein, by preventing cleavage of
PT enzyme

PS Disclosure; Page 2; 64pp; English.

XX This invention relates to a novel method for modulating activity of
CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
CC secretase/shedase. Cleavage of BACE by this enzyme results in the
CC generation of a soluble BACE which enhances the production of the
CC amyloidogenic peptide Abeta which has been shown to be involved in the
CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
CC achieved by administration of an antisense nucleotide molecule capable
CC of hybridising with BACE mRNA, by using a ribozyme that targets and
CC degrades BACE secretase mRNA, with a peptide that can interfere with
CC binding of the enzyme with BACE or using an antibody or antagonist that
CC can function as an inhibitor of BACE secretase activation. The methods
CC of the invention modulate the activity of BACE secretase/shedase by
CC preventing cleavage of BACE, which is useful for the treatment of a
CC neurodegenerative disorder characterised by the generation of Abeta
CC protein, especially Alzheimer's disease. The invention also comprises a
CC method for identification of an agent that can alter the ability of BACE
CC secretase to associate with and process a known substrate, this method
CC can be used for high throughput screening of candidate molecules. The
CC invention also comprises a method for determining whether an individual
CC is at risk of developing a neurodegenerative disorder characterised
CC by the generation of Abeta protein by measuring the levels of BACE
CC C-terminal cleavage products in a sample or tissue where an increase
CC in cleavage products indicates a person at risk. The present sequence
CC represents the beta amyloid precursor protein (APP) beta
CC secretase cleavage site important for beta APP processing.

XX Sequence 6 AA;

Query Match 60.0%; Score 6; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDA 6
| | | | |
Db 1 EVKMDA 6

RESULT 3

AAR37864
ID AAR37864 standard; Protein; 5 AA.

XX AAR37864;

DT 27-OCT-1993 (first entry)

DE Beta-amyloid protein N-terminal peptide deduced from clone SM2W4.

KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
KW neuritic plaque.

OS Homo sapiens.

XX US5220013-A.

XX 15-JUN-1993.

PF 17-NOV-1986; 86US-0932193.

PR 17-NOV-1986; 86US-0932193.

PR 31-DEC-1986; 86US-0948376.

PR 30-JAN-1987; 87US-0008810.

PR 18-AUG-1987; 87US-0087002.

PR 30-NOV-1989; 89US-0444118.

XX (SCIO-) SCIOS NOVA INC.

XX Cordell B, Ponte PA;

XX WPI; 1993-205383/25.

DR N-PSDB; AQA42663.

PT DNA sequence useful for detection of Alzheimer's disease - for
PT encoding beta amyloid core protein
PS Disclosure; Fig 3; 40pp; English.
XX
XX A clone was obtained from the genomic library described in Lawn et al.,
XX Cell, 15;1157-1174 (1978) which included a 57 base pair segment which
XX encodes amino acids 1-18 of the beta-amyloid protein, immediately
XX preceded by a Methionine. A HindIII/RsaI fragment derived from the
XX genomic clone and containing the 57bp segment was used to isolate cDNA
XX fragments from a library prepared from temporal and parietal cortical
XX tissue from a normal human brain. The sequence of one of the
XX isolated clones, designated lambda SM2W4 (see AAQ42663), encodes the
XX Asp-Ala-Glu-Phe amino acids at the amino-terminus of the beta-amyloid
XX protein, preceded by a Met residue.
SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8
DB 1 MDAEF 5
|||||

RESULT 4
AAW08216
ID AAW08216 standard; peptide; 5 AA.
AC AAW08216;
XX
XX 05-SEP-1997 (first entry)
DT Wild type APP beta-cleavage site #1.
DE Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
XX
XX Homo sapiens.
XX WO9640885-A2.
PN 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US09985.
PF 07-JUN-1995; 95US-0485152.
PR 07-JUN-1995; 95US-0480498.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
PA
XX
XX Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI Mcconlogue LC, Sinha S, Tan H;
XX
XX WPI; 1997-052304/05.
XX
XX Beta-secretase which specifically cleaves beta-amyloid precursor
PT protein - useful to screen for inhibitors useful in treatment of
PT Alzheimer's disease
XX
XX Claim 5; Page 59; 92pp; English.
PS
XX
XX AAW08216, AAW08217 and AAW08350 represent beta-cleavage sites from
CC beta-amyloid precursor proteins (APP). These sequences are recognised by
CC the enzyme of the invention. The enzyme of the invention is
CC beta-secretase, and specifically cleaves beta-APP at one of these sites.
CC Normal processing of beta-APP is thought to occur via cleavage between
CC residues 16 and 17 of the beta-amyloid peptide region by an
CC alpha-secretase. Pathogenic processing is thought to occur by
CC beta-secretase cleavage of beta-APP. Beta-secretase activity can be
CC detected and measured using a method of the invention, which detects at

CC least one of the beta-secretase cleavage products formed on cleavage. The
CC method can be used to determine whether a test substance inhibits
CC proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective
CC to at least partially inhibit beta-secretase activity can be used to
CC inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and
CC purification of beta-secretase will permit chemical modelling of a
CC critical event in the pathology of Alzheimer's disease.
XX
SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
DB 1 VKMDA 5
|||||

RESULT 5
AAW61150
ID AAW61150 standard; Peptide; 5 AA.
AC AAW61150;
XX
XX 26-OCT-1998 (first entry)
DT Wild-type APP cleavage site.
DE Beta-secretase; human; beta-amyloid precursor protein; APP;
KW protease; inhibitor; screening; Alzheimer's disease; therapy.
XX
XX Homo sapiens.
XX WO9826059-A1.
PN 18-JUN-1998.
XX
XX 11-DEC-1996; 96WO-US19549.
PF 11-DEC-1996; 96WO-US19549.
PR (ATHE-) ATHENA NEUROSCIENCES INC.
XX
XX Anderson JP, Chrysler SMS, Keim PS, Sinha S;
PI WPI; 1998-348519/30.
XX
XX Novel beta-secretase which cleaves beta-amyloid precursor protein -
PT useful for screening for compounds which inhibit the cleavage and
PT are useful for treating Alzheimer's disease
XX
XX Disclosure; Page 20; 39pp; English.
XX
XX This peptide comprises the site of wild-type beta-amyloid precursor
CC protein (APP) (MBP-Cl25 WT) that is cleaved by a novel
CC beta-secretase isolated from human 293 cells. This protease
CC cleaves APP at the N-terminus of the beta-amyloid peptide (beta-AP).
CC It is believed to be the putative beta-secretase responsible for
CC the pathogenic processing of APP to beta-AP in Alzheimer's disease,
CC Down's syndrome and HCHWA-D. Recombinant fusion proteins were
CC generated comprising the last 125 amino acids of APP (wild-type
CC or Swedish double mutation, see AAW61151-52) fused to the C-terminal
CC end of maltose binding protein. The 2 fusion proteins were
CC expressed in Escherichia coli, and used as substrates for
CC beta-secretase in beta-secretase inhibitor assays. Compounds that
CC inhibit APP cleavage by beta-secretase may be useful in the
XX treatment of Alzheimer's disease.
XX
SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
|||||
Db 1 VKMDA 5

RESULT 6

AAY33750
ID AAY33750 standard; Protein; 5 AA.

XX AAY33750;

AC 09-NOV-1999 (first entry)

DT Wild type beta-amyloid protein precursor (APP) cleavage site.

DE Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW Alzheimer's disease; cleavage site; wild type.

XX Homo sapiens.

OS US5942400-A.

PN 24-AUG-1999.

XX 07-JUN-1996; 96US-0659984.

XX 07-JUN-1996; 96US-0659984.

PR 07-JUN-1995; 95US-0480498.

PR 07-JUN-1995; 95US-0485152.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Jacobson-Croak KL, Sinha S;

PI WPI; 1999-517417/43.

XX A method for detecting human beta-secretase cleavage of polypeptides
PT useful for identifying beta-secretase inhibitors

XX Examples; Column 28; 43pp; English.

XX This sequence is the wild type beta-amyloid protein precursor (APP)
CC cleavage site. APP is cleaved by beta-secretase AAY33741. The wild type
CC cleavage site and the Swedish mutant version of this site AAY33751 are
CC used in a method for detecting human beta-secretase cleavage of
CC polypeptides and for identifying beta-secretase inhibitors. Inhibition
CC of beta-secretase activity would be useful for chemical modelling of a
CC critical event in the pathology of Alzheimer's disease. Inhibitors of
CC beta-secretase would be useful for the prevention and treatment of
CC Alzheimer's disease and Down's Syndrome.

XX Sequence 5 AA;

Query Match 50.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
|||||
Db 1 VKMDA 5

RESULT 7

AAY08608
ID AAY08608 standard; Protein; 5 AA.

XX AAY08608;

AC 05-AUG-1999 (first entry)

DT Human NSE promoter protein fragment.

XX

KW APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
KW Alzheimer's disease; model; therapeutic compound; brain; mechanism;
KW nerve tissue specific promoter; synthesis; inhibitor; deposition;
KW plaque formation; treatment; NSE promoter.

XX Homo sapiens.

OS US5912410-A.

PN 15-JUN-1999.

PD 13-APR-1995; 95US-0422333.

XX 21-OCT-1994; 94US-0327381.

XX 15-JUN-1990; 90US-0538857.

PR 17-JUN-1991; 91US-0716725.

PR 13-APR-1995; 95US-0422333.

XX (SCIO-) SCIOS INC.

PA Cordell B;

XX WPI; 1999-357231/30.

DR N-PSDB; AAX77497.

XX Transgenic mice useful for studying compounds potentially useful in
PT the treatment of Alzheimer's disease

XX Disclosure; Fig 4B; 72pp; English.

XX This invention describes novel transgenic mice expressing proteins
CC related to the pathology of Alzheimer's disease and which provide models
CC for studying potentially therapeutic compounds. The transgenic mice
CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)
CC and a nerve tissue specific promoter operably linked to the beta-APP
CC allowing its expression to form beta-amyloid protein deposits in the
CC animal's brain. The transgenic mouse is useful for elucidating the
CC molecular mechanisms involved in the synthesis of and, more importantly,
CC inhibiting the synthesis and deposition of beta-amyloid proteins (most
CC importantly in the brain where plaque formation is associated with
CC Alzheimer's disease) by inhibiting production and/or increasing cleavage
CC after production. The transgenic animals provide useful models for
CC studying the in vivo relationships of the proteins to each other and to
CC other compounds being tested for their usefulness in treating Alzheimer's
CC disease.

XX Sequence 5 AA;

Query Match 50.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8
|||||

Db 1 MDAEF 5

RESULT 8

AAY69702
ID AAY69702 standard; peptide; 5 AA.

XX AAY69702;

AC 11-APR-2000 (first entry)

DT Beta-APP alpha-secretase substrate APP(1,+5).

XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW cleavage site; beta-secretase; neurodegenerative disease;
KW Alzheimer's disease.

XX Homo sapiens.

```

XX PN WO9964587-A1.
XX PD 16-DEC-1999.
XX PF 04-JUN-1999; 99WO-FR01326.
XX PR 05-JUN-1998; 98FR-0007068.
XX PR 31-MAR-1999; 99US-0122599.
XX PA (RHON ) RHONE-POULENC RORER SA.
XX PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX PI Rhoham M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX DR WPI; 2000-097537/08.
XX PT Polypeptide with beta-secretase activity, specific for wild-type
XX PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX PS Example 3; Page 24; 44pp; French.
XX CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
XX CC novel polypeptide with beta-secretase activity that can cleave
XX CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
XX CC cleavage of the protein occurs between amino acids Met596-Asp597 and
XX CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
XX CC polypeptide is used to identify agents that interact specifically with
XX CC it. These agents regulate metabolism of APP, particularly they slow down
XX CC or reduce production of beta-amyloid, so can be used to treat
XX CC neurodegenerative diseases, particularly Alzheimer's disease.
XX SQ Sequence 5 AA;
Query Match 50.0%; Score 5; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DAEFR 9
Db 1 DAEFR 5
RESULT 9
ID AAE10667
XX AAE10667 standard; peptide; 5 AA.
XX AC AAE10667;
XX DT 10-DEC-2001 (first entry)
XX DE Human APP-Sw mutant beta-secretase substrate peptide #1.
XX KW Human; aspartyl protease 1; Asp1; amyloid precursor protein;
XX KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX KW amyloid plaque; neuronal loss; proteolytic; neuroprotective;
XX KW APP-Sw beta-secretase peptide; mutant; mutein.
XX OS Homo sapiens.
XX PN GB2357767-A.
XX PD 04-JUL-2001.
XX PF 22-SEP-2000; 2000GB-0023315.
XX PR 23-SEP-1999; 99US-0155493.
XX PR 23-SEP-1999; 99US-0404133.
XX PR 23-SEP-1999; 99WO-US20881.
XX PR 13-OCT-1999; 99US-0416901.
XX PR 06-DEC-1999; 99US-0169232.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Bienkowski MJ, Gurney M;
XX DR WPI; 2001-444208/48.
XX PT Polypeptide comprising fragments of human aspartyl protease with
XX PT amyloid precursor protein processing activity and alpha-secretase
XX PT activity, for identifying modulators useful in treating Alzheimer's
XX PT disease -
XX PS Example 12; Page 84; 187pp; English.
XX CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
XX CC Asp1 proteins which lack transmembrane domain or amino terminal
XX CC domain or cytoplasmic domain and retains alpha-secretase activity
XX CC and amyloid protein precursor (APP) processing activity. The proteins
XX CC of the invention are useful for assaying hu-Asp1 alpha-secretase
XX CC activity, which in turn is useful for identifying modulators of
XX CC hu-Asp1 alpha-secretase activity, where modulators that increase
XX CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
XX CC disease (AD) which causes progressive dementia with consequent
XX CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
XX CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
XX CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
XX CC the substrate under acidic conditions and determining the level of
XX CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
XX CC precursor protein-Swedish (APP-Sw) mutant beta-secretase specific
XX CC substrate peptide. This peptide is obtained by Swedish KM-NL mutation
XX CC of human APP protein. This peptide is used for assaying the beta-
XX CC secretase activity of human Aspartyl protease 2a (Asp2a) protein.
XX CC The peptide is also used for determining the relationship between
XX CC Asp1 and APP protein.
XX SQ Sequence 5 AA;
Query Match 50.0%; Score 5; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DAEFR 9
Db 1 DAEFR 5
RESULT 10
ID AAE06907
XX AAE06907 standard; peptide; 5 AA.
XX AC AAE06907;
XX DT 23-OCT-2001 (first entry)
XX DE Human Asp-2 beta-secretase activity assaying substrate peptide #1.
XX KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
XX KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
XX KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neuroprotective;
XX KW neuroprotective; antisense therapy; gene therapy.
XX OS Synthetic.
XX PN WO200150829-A2.
XX PD 19-JUL-2001.
XX PF 09-MAY-2001; 2001WO-IB00799.
XX PR 09-MAY-2001; 2001WO-IB00799.
XX PA (BIEN/) BIENKOWSKI M J.
XX PA (GURN/) GURNEY M E.
XX PA (HEIN/) HEINRIKSON R L.
XX PA (PARO/) PARODI L A.

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PA (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 PI WPI; 2001-483072/52.
 DR Novel purified polypeptide comprising fragment of mammalian aspartyl
 XX protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX Example 12; Page 80; 185pp; English.
 PS The invention relates to a purified polypeptide comprising a fragment of
 XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of beta processing is useful in
 CC assays relating to the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is one of the
 CC products of Asp 2 degradation on the peptide sequence appearing as
 CC AAU06627.
 XX Sequence 5 AA;
 SQ Query Match 50.0%; Score 5; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DAEFR 9
 Db 1 DAEFR 5
 |||||
 RESULT 11
 AAU06636
 ID AAU06636 standard; Peptide; 5 AA.
 AC AAU06636;
 XX 24-OCT-2001 (first entry)
 DT Peptide product of Asp2 activity #1.
 XX Aspartyl protease; Asp2; beta-secretase; neurotropic;
 DE neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta.
 XX Synthetic.
 OS WO200149098-A2.
 XX WO200149098-A2.
 PN 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-IB00798.
 PF 09-MAY-2001; 2001WO-IB00798.
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 PI WPI; 2001-502549/55.
 DR Novel purified polypeptide comprising fragment of mammalian aspartyl
 XX protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX Example 12; Page 80; 185pp; English.
 PS The invention relates to a purified polypeptide comprising a fragment of
 XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of beta processing is useful in
 CC assays relating to the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is one of the
 CC products of Asp 2 degradation on the peptide sequence appearing as
 CC AAU06627.
 XX Sequence 5 AA;
 SQ Query Match 50.0%; Score 5; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DAEFR 9
 Db 1 DAEFR 5
 |||||
 RESULT 12
 AAU07235
 ID AAU07235 standard; Peptide; 5 AA.
 AC AAU07235;
 XX 24-OCT-2001 (first entry)
 DT Human beta-amyloid protein precursor, APP-beta secretase site peptide #5.
 DE Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 XX beta-secretase; Alzheimer's disease; APP-beta.
 OS Homo sapiens.
 XX WO200149097-A2.
 PN 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-IB00797.
 PF 09-MAY-2001; 2001WO-IB00797.
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI; 2001-502548/55.
 DR
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity
 XX
 XX Example 12; Page 80; 185pp; English.
 PS
 XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP-beta
 CC secretase site peptide substrate #5 used in assays of human Asp2 beta-
 CC secretase activity.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 50.0%; Score 5; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DAEPF 9
 DB 1 DAEPF 5
 |||||

RESULT 13
 AAB47260
 ID AAB47260 standard; Peptide; 5 AA.
 XX AAB47260;
 AC
 XX
 XX 18-JUL-2001 (first entry)
 DT
 XX
 XX Wild type APP sequence for cleavage by beta-secretase.
 DE
 XX
 XX Beta-secretase; isotype; beta-amyloid precursor protein; APP;
 KW beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
 KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.
 XX
 XX Homo sapiens.
 OS
 XX US6221645-B1.
 PN
 XX 24-APR-2001.
 PD
 XX 07-JUN-1996; 96US-0660531.
 PF
 XX 07-JUN-1995; 95US-0480498.
 PR

XX (ELAN-) ELAN PHARM INC.
 PA
 XX Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
 PI
 XX WPI; 2001-315578/33.
 DR
 XX
 XX Novel antibody that specifically binds native beta-secretase protein,
 PT useful for raising anti-idiotypic antibodies and for detecting or
 PT diagnosing pathological conditions related to presence of respective
 PT antigens
 XX
 XX Example; Column 28; 42pp; English.
 PS
 XX The sequences given in AAB47260-61 represent cleavage sites derived
 CC from wild-type and the Swedish mutation of beta-amyloid precursor
 CC protein (APP). These cleavage sites were used in fusion proteins
 CC which were used as substrates for the beta-secretase protein which
 CC is characterized by an ability to cleave the 695-amino acid isotype
 CC of APP between amino acids 596 and 597. The fusion proteins contain
 CC the carboxy-terminal end of Maltose binding protein (MBP) fused to
 CC the carboxy-terminal 125 amino acids of either wild type APP or APP
 CC containing the Swedish mutation. Beta-secretase is thought to be
 CC responsible for the pathogenic processing of APP to form beta amyloid
 CC peptide (beta-AP) in beta-AP related conditions, e.g. Alzheimer's
 CC disease, Downs syndrome, HCHWA-D etc. Beta-secretase has a molecular
 CC weight of 260-300 kD and will bind to wheat germ agglutinin but not to
 CC concanavalin A. Beta-secretase will cleave both the wild type and
 CC the Swedish mutation of APP.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 50.0%; Score 5; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
 DB 1 VKMDA 5
 |||||

RESULT 14
 ABB06534
 ID ABB06534 standard; Peptide; 5 AA.
 XX ABB06534;
 AC
 XX
 XX 31-MAY-2002 (first entry)
 DT
 XX
 XX Beta-secretase related peptide SEQ ID NO:129.
 DE
 XX
 XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX WO200206306-A2.
 PN
 XX
 XX 24-JAN-2002.
 PD
 XX
 XX 19-JUL-2001; 2001WO-US23035.
 PF
 XX
 XX 19-JUL-2000; 2000US-219795P.
 PR
 XX 12-MAR-2001; 2001US-275251P.
 PR
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA
 XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;
 XX WPI; 2002-216995/27.
 DR

XX Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease -
XX Disclosure; Page 166; 188pp; English.
XX The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 5 AA;
Query Match 50.0%; Score 5; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KMDAE 7
| | | | |
Db 1 KMDAE 5
RESULT 15
ABB06579
ID ABB06579 standard; Peptide; 5 AA.
XX
AC ABB06579;
XX
DT 31-MAY-2002 (first entry)
DE
DE Amyloid protein precursor peptide SEQ ID NO:180.
XX
KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200206306-A2.
XX
PD 24-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23035.
XX
XX 19-JUL-2000; 2000US-219795P.
PR
PR 12-MAR-2001; 2001US-275251P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
XX WPI; 2002-216995/27.
XX
XX Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease -
XX
XX Example 8; Page 90; 188pp; English.
XX
XX The present invention describes an isolated peptide (I) comprising a

CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 5 AA;
Query Match 50.0%; Score 5; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VKMDA 6
| | | | |
Db 1 VKMDA 5
Search completed: April 21, 2003, 12:14:16
Job time : 35 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:43 : Search time 23.5 seconds
(without alignments)
87.680 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFHDSGYE 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1223

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SPTREMBL 21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	13 Q9PS69	Q9PS69 gallus faml
2	3	30.0	10	6 Q9TU33	Q9TU33 canis faml
3	3	30.0	10	10 P81899	P81899 prunus dulc
4	3	30.0	10	12 Q9JIG8	Q9JIG8 tt virus. o
5	2	20.0	7	2 Q47477	Q47477 escherichia
6	2	20.0	7	4 Q15897	Q15897 homo sapien
7	2	20.0	7	6 Q28742	Q28742 oryctolagus
8	2	20.0	7	8 Q98866	Q98866 spinacia ol
9	2	20.0	8	2 Q68485	Q68485 klebsiella
10	2	20.0	8	2 Q9X3K1	Q9X3K1 prochloroco
11	2	20.0	8	2 Q9S6D5	Q9S6D5 escherichia
12	2	20.0	8	2 P72221	P72221 pseudomonas
13	2	20.0	8	2 Q9R7T2	Q9R7T2 escherichia
14	2	20.0	8	2 Q9RSR2	Q9RSR2 shigella dy
15	2	20.0	8	2 Q9R3X0	Q9R3X0 planktothri
16	2	20.0	8	2 Q9R5L7	Q9R5L7 clostridium

17	2	20.0	8	2	Q8RSR3	Q8rsr3 lactobacill
18	2	20.0	8	4	Q9UJ50	Q9uj50 homo sapien
19	2	20.0	8	4	Q15901	Q15901 homo sapien
20	2	20.0	8	4	Q9V4J4	Q9v4j4 homo sapien
21	2	20.0	8	4	Q16428	Q16428 homo sapien
22	2	20.0	8	4	Q60773	Q60773 homo sapien
23	2	20.0	8	5	Q94623	Q94623 manduca sex
24	2	20.0	8	5	Q9TWH6	Q9twh6 perinerels
25	2	20.0	8	6	Q9MYL5	Q9myl5 pongo pygma
26	2	20.0	8	6	Q9GMH3	Q9gmh3 lagenorhync
27	2	20.0	8	6	Q28866	Q28866 megaptera n
28	2	20.0	8	6	Q8WNS1	Q8wns1 bos taurus
29	2	20.0	8	6	Q9BFC3	Q9bfc3 didelphis m
30	2	20.0	8	6	Q9BFC2	Q9bfc2 macropus eu
31	2	20.0	8	6	Q9BFC1	Q9bfc1 choleopus h
32	2	20.0	8	6	Q9BFC0	Q9bfc0 choleopus d
33	2	20.0	8	6	Q9BFB9	Q9bfb9 euphractus
34	2	20.0	8	6	Q9BFB8	Q9bfb8 chaetophrac
35	2	20.0	8	6	Q9BFB7	Q9bfb7 tamarandua te
36	2	20.0	8	6	Q9BFB6	Q9bfb6 myrmecophag
37	2	20.0	8	6	Q9BFB5	Q9bfb5 erinaceus c
38	2	20.0	8	6	Q9BFB4	Q9bfb4 talpa alta
39	2	20.0	8	6	Q9BFB3	Q9bfb3 condylura c
40	2	20.0	8	6	Q9BFB2	Q9bfb2 sorex arane
41	2	20.0	8	6	Q9BFB1	Q9bfb1 echinops te
42	2	20.0	8	6	Q9BEB0	Q9beb0 trichechus
43	2	20.0	8	6	Q9BFA9	Q9bfa9 procavia ca
44	2	20.0	8	6	Q9BFA8	Q9bfa8 loxodonta a
45	2	20.0	8	6	Q9BFA7	Q9bfa7 macrosceili

ALIGNMENTS

RESULT 1

Q9PS69 PRELIMINARY; PRT; 8 AA.
ID Q9PS69
AC Q9PS69;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 265:19079-19087(1991).
FT NON_TER 1 8
FT NON_TER 1 8
SQ SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;

Query Match 30.0%; Score 3; DB 13; Length 8;

Best Local Similarity 100.0%; Pred. No. 6.7e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSG 8

Db 2 DSG 4

RESULT 2

Q9TU33 PRELIMINARY; PRT; 10 AA.
ID Q9TU33
AC Q9TU33;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE BRCA1 (Fragment).
 GN BRCA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20154965; PubMed=10690375;
 RA Gray I.S., Yuzbasiyan-Gurkan V.;
 RT "A single nucleotide (T->G) polymorphism within intron 23 of the
 RT canine BRCA1 gene.";
 RL Anim. Genet. 31:76-77(2000).
 DR EMBL; AF159258; AAD56289.1;
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;
 Query Match 30.0%; Score 3; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 DSG 8
 Db 6 DSG 8
 RESULT 3
 ID P81899 PRELIMINARY; PRT; 10 AA.
 AC P81899;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large
 DE chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
 DE glycosidase) (N-glycanase) (Fragment).
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RX PubMed=9523720;
 RA Altmann F., Paschinger K., Dalik T., Vorauer K.;
 RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
 RT amidase A and its N-glycans.";
 RL Eur. J. Biochem. 252:118-123(1998).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
 CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
 CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
 CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
 CC CONTAINING AN ASPARTIC RESIDUE.
 CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
 CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
 CC DEGLYCOSYLATION.
 CC -1- MASS SPECTROMETRY: MW=54182; METHOD=MALDI-MS.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;
 Query Match 30.0%; Score 3; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SGY 9
 Db 3 SGY 5

RESULT 4
 Q9J1G8
 ID Q9J1G8 PRELIMINARY; PRT; 10 AA.
 AC Q9J1G8;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE ORF2.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TTV-SC232;
 RA MEDLINE=20251008; PubMed=10790123;
 RA Niel C., Saback F.L., Lampe E.;
 RT "Coinfection with Multiple TT Virus Strains Belonging to Different
 RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
 RL J. Clin. Microbiol. 38:1926-1930(2000).
 DR EMBL; AF216453; AAF66889.1;
 SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;
 Query Match 30.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEF 3
 Db 2 AEF 4
 RESULT 5
 ID Q47477 PRELIMINARY; PRT; 7 AA.
 AC Q47477;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE Tpi protein (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE OF 7-7 FROM N.A.
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellinga H.W., Evans P.R.;
 RT "Nucleotide sequence and high-level expression of the major
 RT Escherichia coli phosphofructokinase.";
 RL Eur. J. Biochem. 149:363-373(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Evans P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X02519; CAA26359.1;
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;
 Query Match 20.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AE 2
 Db 1 AE 2
 RESULT 6
 Q15897
 ID Q15897 PRELIMINARY; PRT; 7 AA.
 AC Q15897;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coilbaugh M.L., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: L32077; AAA73887.1; -.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 20.0%; Score 2; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2
 Db 5 AE 6

RESULT 7
 Q28742
 ID Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL: K01698; AAA31415.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 20.0%; Score 2; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HD 6
 Db 4 HD 5

RESULT 8
 Q98866
 ID Q98866 PRELIMINARY; PRT; 7 AA.
 AC Q98866;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Cytochrome b/f subunit IV (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86120353; PubMed=3003688;
 RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
 RT protein S11 and RNA polymerase alpha-subunit";
 RL Nucleic Acids Res. 14:1029-1044(1986).
 DR EMBL: X03496; CAA27215.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 20.0%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FR 4
 Db 2 FR 3

RESULT 9
 O68485
 ID O68485 PRELIMINARY; PRT; 8 AA.
 AC O68485;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
 GN AADAL.
 OS Klebsiella pneumoniae.
 OG Plasmid pIQ1000.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=98287600; PubMed=9624504;
 RA Centron D., Roy P.H.;
 RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
 RT aac(6)-Iq from the integron of a natural multiresistance plasmid";
 RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
 DR EMBL: AF047556; AAC25501.1; -.
 KW Plasmid; Transferase.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2
 Db 3 AE 4

RESULT 10
 Q9X3K1
 ID Q9X3K1 PRELIMINARY; PRT; 8 AA.
 AC Q9X3K1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Cytochrome b (Fragment).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.

```
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070193; AAD23233.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 799 MW; 10376865B7286603 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
Db 5 SG 6

RESULT 11
Q9S6D5 PRELIMINARY; PRT; 8 AA.
AC Q9S6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative is30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Rahn A., Drummelsmith J., Whitefield C.;
RT "Conserved organization in the cps gene clusters for expression of
RT Escherichia coli group 1 k antigens: relationship to the colanic acid
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DCLA9D1B41406 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
Db 7 AE 8

RESULT 12
P72221 PRELIMINARY; PRT; 8 AA.
AC P72221;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alginatase lyase (Fragment).
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (Oct-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=OS-ALG-9;
RX MEDLINE=93329366; PubMed=8336113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an alginatase lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38469; BAA21704.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
Db 7 AE 8

RESULT 13
Q9R7T2 PRELIMINARY; PRT; 8 AA.
AC Q9R7T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996).
DR EMBL; D90703; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
Db 5 AE 6

RESULT 14
Q9R5R2 PRELIMINARY; PRT; 8 AA.
AC Q9R5R2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 31,000 DA product of ORF6 (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=622;
```

```
RN SEQUENCE.
RP MEDLINE=92085268; PubMed=1660923;
RA Polard P., Priere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
RL in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 902 MW; FE2DCAF586AE336 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GY 9
  ||
DB 4 GY 5

RESULT 15
Q9R3X0
ID Q9R3X0 PRELIMINARY; PRT; 8 AA.
AC Q9R3X0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Planktotothrix rubescens.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktotothrix.
OX NCBI_TaxID=59512;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, AND BC-PLA 9303;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
RT "The diversity of gas vesicle genes in Planktotothrix rubescens from
RT Lake Zurich.";
RL Microbiology 145:2757-2768(1999).
DR EMBL; AJ132249; CAB59537.1; -.
DR EMBL; AJ132248; CAB59534.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 957 MW; 33D1AAA685BB19CB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
  ||
DB 1 EF 2

Search completed: April 21, 2003, 12:41:58
Job time : 23.5 secs
```


GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:13 ; Search time 13 Seconds
(without alignments)
73.950 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFRRHDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1014

Minimum DB seq length: 5
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3	30.0	5	A26830	mitosis inhibiting
2	3	30.0	8	S78036	ribosomal protein
3	3	30.0	10	A59272	peptide-N4-(N-acet
4	3	30.0	10	PT0243	Ig heavy chain CRD
5	3	30.0	10	PT0215	T-cell receptor be
6	3	30.0	10	PH0900	T-cell receptor be
7	2	20.0	5	A41225	copper resistance
8	2	20.0	5	B41225	copper resistance
9	2	20.0	5	D60274	major protein anti
10	2	20.0	5	B37988	acid proteinase li
11	2	20.0	5	A44692	fulicin - giant Af
12	2	20.0	5	JT0520	Ig kappa chain V-I
13	2	20.0	5	D44823	synaptosomal-assoc
14	2	20.0	5	PT0513	T-cell receptor be
15	2	20.0	5	PT0600	T-cell receptor be
16	2	20.0	5	PT0608	T-cell receptor be
17	2	20.0	5	PT0669	T-cell receptor be
18	2	20.0	5	PT0553	T-cell receptor be
19	2	20.0	5	PT0538	T-cell receptor be
20	2	20.0	5	PT0540	T-cell receptor be
21	2	20.0	5	PT0703	T-cell receptor be
22	2	20.0	5	PT0690	T-cell receptor be
23	2	20.0	5	PT0707	T-cell receptor be
24	2	20.0	5	PT0573	T-cell receptor be
25	2	20.0	5	PT0572	T-cell receptor be
26	2	20.0	5	PT0579	T-cell receptor be
27	2	20.0	5	PT0701	T-cell receptor be
28	2	20.0	5	PT0717	T-cell receptor be
29	2	20.0	6	S02617	alcohol dehydrogen

30	2	20.0	6	A61411	ameletin - rat
31	2	20.0	6	JU0355	lipopeptide WS1279
32	2	20.0	6	S29637	jacalin beta-II ch
33	2	20.0	6	A60494	antineoplastic gly
34	2	20.0	6	I51434	H4 histone - Afric
35	2	20.0	6	PT0280	Ig heavy chain CRD
36	2	20.0	6	PT0629	T-cell receptor be
37	2	20.0	6	PT0511	T-cell receptor be
38	2	20.0	6	PT0514	T-cell receptor be
39	2	20.0	6	PT0516	T-cell receptor be
40	2	20.0	6	PT0532	T-cell receptor be
41	2	20.0	6	PT0512	T-cell receptor be
42	2	20.0	6	PT0604	T-cell receptor be
43	2	20.0	6	PT0630	T-cell receptor be
44	2	20.0	6	PT0605	T-cell receptor be
45	2	20.0	6	PT0687	T-cell receptor be

ALIGNMENTS

RESULT 1

A26830
mitosis inhibiting peptide - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A26830
R;Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A:Reference number: A26830; MUID:87298602; PMID:3619940
A:Accession: A26830
A:Molecule type: protein
A:Residues: 1-5 <REI>
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; pyrrolutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSG 8
|||
Db 3 DSG 5

RESULT 2

S78036
ribosomal protein Yms-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C:Species: Saccharomyces cerevisiae
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C:Accession: S78036
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wit
Eur. J. Biochem. 245, 449-456, 1997
A:Title: Identification and characterization of the genes for mitochondrial ribosomal
A:Reference number: S78018; MUID:97296414; PMID:9151978
A:Accession: S78036
A:Molecule type: protein
A:Residues: 1-8 <KIT>
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSG 8
|||
Db 6 DSG 8

RESULT 3

A59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52); A, large chain
N; Alternate names: peptide N-glycosidase
C; Species: Prunus dulcis var. sativa (sweet almond)
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C; Accession: A59272
R; Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A; Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase
A; Reference number: A59272; MUID:98181894; PMID:9523720
A; Accession: A59272
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-10 <ALT>
C; Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGY 9
|||
Db 3 SGY 5

RESULT 4

PT0243
Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PT0243
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A; Reference number: PT0222; MUID:91108337; PMID:1899102
A; Accession: PT0243
A; Molecule type: DNA
A; Residues: 1-10 <YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGY 9
|||
Db 7 SGY 9

RESULT 5

PT0215
T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C; Accession: PT0215
R; Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A; Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A; Reference number: PT0209; MUID:91217621; PMID:1902501
A; Accession: PT0215
A; Molecule type: mRNA
A; Residues: 1-10 <NAK>
C; Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GYE 10
|||
Db 5 GYE 7

RESULT 6

PH0900
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C; Accession: PH0900
R; Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A; Reference number: PH0891; MUID:92078857; PMID:1836012
A; Accession: PH0900
A; Molecule type: mRNA
A; Residues: 1-10 <GOL>
A; Experimental source: myelin basic protein-immunized T-cell
C; Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DSG 8
|||
Db 5 DSG 7

RESULT 7

A41225
copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)
C; Species: Pseudomonas syringae pv. tomato
C; Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C; Accession: A41225
R; Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A; Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A; Reference number: A41225; MUID:92020961; PMID:1924351
A; Accession: A41225
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
||
Db 2 SG 3

RESULT 8

B41225
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C; Species: Pseudomonas syringae pv. tomato
C; Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C; Accession: B41225
R; Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A; Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A; Reference number: A41225; MUID:92020961; PMID:1924351
A; Accession: B41225
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
||
Db 1 AE 2

RESULT 9

D60274
 major protein antigen MP46 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: D60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the culture
 A:Reference number: A60274; MUID:9109989; PMID:1898899
 A:Accession: D60274
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DS 7
 ||
 Db 2 DS 3

RESULT 10

B37988
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C:Species: Physarum polycephalum
 C>Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 C:Accession: B37988
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og
 J. Biol. Chem. 265, 19898-19903, 1990
 A:Title: Purification and characterization of a novel intracellular acid proteinase from
 A:Reference number: A37988; MUID:91060608; PMID:2246266
 A:Accession: B37988
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
 ||
 Db 1 AE 2

RESULT 11

A44692
 fulicin - giant African snail
 C:Species: Achatina fulica (giant African snail)
 C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
 C:Accession: A44692
 R:Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No
 Biochem. Biophys. Res. Commun. 178, 486-493, 1991
 A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
 A:Reference number: A44692; MUID:91315471; PMID:1859408
 A:Accession: A44692
 A:Molecule type: protein
 A:Residues: 1-5 <OHT>
 C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
 F:2/Modified site: D-asparagine (Asn) #status experimental
 F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
 ||
 Db 3 EF 4

RESULT 12

JT0520
 Ig kappa chain V-III region (SDI) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
 C:Accession: JT0520
 R:Anker, R.; Conley, M.E.; Pollok, B.A.
 J. Exp. Med. 169, 2109-2119, 1989
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglob
 A:Reference number: JT0511; MUID:89279157; PMID:2786547
 A:Accession: JT0520
 A:Molecule type: mRNA
 A:Residues: 1-5 <ANK>
 A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangeme
 A>Note: a stop codon terminates the sequence in the V region
 C:Keywords: heterotrimer; immunoglobulin
 F:1-5/Domain: V kappa region <VRE>

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
 ||
 Db 3 SG 4

RESULT 13

D44823
 synaptosomal-associated protein SNAP-25 peptide 2 - rabbit (fragment)
 N:Alternate names: superprotein peptide 2
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
 C:Accession: D44823
 R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.
 J. Neurosci. 11, 3412-3421, 1991
 A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein)
 A:Reference number: A44823; MUID:92044785; PMID:1941090
 A:Accession: D44823
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <LOE>
 A:Experimental source: visual tissue
 A>Note: sequence extracted from NCBI backbone (NCBIP:64250)
 C:Keywords: membrane trafficking

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
 ||
 Db 4 SG 5

RESULT 14

PT0513
 T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0513; PT0606
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0513
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL
 A:Accession: PT0606
 A>Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-5 <PE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
 ||
Db 2 SG 3

RESULT 15
PT0600
T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0600
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711538
A:Accession: PT0600
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DS 7
 ||
Db 4 DS 5

Search completed: April 21, 2003, 12:42:31
Job time : 14 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:02 : Search time 7 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFHDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2	20.0	5	1 RE21_LITRU	P82071 litoria rub
2	2	20.0	5	1 RE31_LITRU	P82072 litoria rub
3	2	20.0	5	1 UX44_CHLTR	P38005 chlamydia t
4	2	20.0	6	1 FARP_MONEX	P41966 moniezia ex
5	2	20.0	6	1 TRPI_PSEPU	P36414 pseudomonas
6	2	20.0	6	1 UN06_CLOPA	P81351 clostridium
7	2	20.0	7	1 E105_LITRU	P82101 litoria rub
8	2	20.0	7	1 FARI_ASCSU	P31889 ascaris suu
9	2	20.0	7	1 UF03_MOUSE	P38641 mus musculu
10	2	20.0	8	1 AL17_CARMA	P81820 carcinus ma
11	2	20.0	8	1 ALL5_CYPFO	P82156 cydia pomon
12	2	20.0	8	1 CPD1_ENTFA	P13269 enterococcu
13	2	20.0	8	1 GLUR_HUMAN	P02729 homo sapien
14	2	20.0	8	1 LCK5_LEUMA	P19987 leucophaea
15	2	20.0	8	1 PK3_PERAM	P82618 periplaneta
16	2	20.0	8	1 UC26_MAIZE	P80632 zea mays (m
17	2	20.0	8	1 VGLG_HSV2B	P81780 herpes simp
18	2	20.0	9	1 COXE_THUOB	P80975 thunnus obe
19	2	20.0	9	1 DSIP_RABIT	P01158 oryctolagus
20	2	20.0	9	1 FARI_ASCSU	P43170 ascaris suu
21	2	20.0	9	1 FARP_CALVO	P41861 calliphora
22	2	20.0	9	1 FARP_CALST	P38495 callinectes
23	2	20.0	9	1 FIBB_MACFU	P19345 macaca fusc
24	2	20.0	9	1 FIBB_PAPAN	P19344 papio anubi
25	2	20.0	9	1 MOSF_CLYJA	P19853 clypeaster
26	2	20.0	9	1 MOSH_CLYJA	P19852 clypeaster
27	2	20.0	9	1 NEUU_CAVPO	P34966 cavia porce
28	2	20.0	9	1 NEUX_HUMAN	P04277 homo sapien
29	2	20.0	9	1 OXYT_OCTVU	P80027 octopus vul
30	2	20.0	9	1 TKL1_LOCM1	P16223 locusta mig
31	2	20.0	9	1 TRP4_LEUMA	P81736 leucophaea
32	2	20.0	9	1 XVIA_STRSQ	P19149 streptomyce
33	2	20.0	10	1 COXO_RAT	P80432 rattus norv

34	2	20.0	10	1 COXQ_THUOB	P80982 thunnus obe
35	2	20.0	10	1 COXQ_RABIT	P80336 oryctolagus
36	2	20.0	10	1 CU30_LOCM1	P11735 locusta mig
37	2	20.0	10	1 ESTA_SCHGA	P81012 schizaphis
38	2	20.0	10	1 FARP_MYTED	P42560 mytilus edu
39	2	20.0	10	1 FIBB_CERST	P14337 ceratotheri
40	2	20.0	10	1 GAJU_HUMAN	P01358 homo sapien
41	2	20.0	10	1 GLEM_HUMAN	P02728 homo sapien
42	2	20.0	10	1 GON3_PETMA	P30948 petromyzon
43	2	20.0	10	1 HTF_HELZE	P16353 heliothis z
44	2	20.0	10	1 HTF_TABAT	P14596 tabanus atr
45	2	20.0	10	1 MOSQ_CLYJA	P19962 clypeaster

ALIGNMENTS

RESULT 1
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC -!- ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
DB 2 EF 3

RESULT 2
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC -!- ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).

CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.

KW Amphibian skin; Amidation.

FT MOD_RES 5 5 AMIDATION.

SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3

DB 2 EF 3

RESULT 3

UXA4_CHLTR

ID UXA4_CHLTR STANDARD; PRT; 5 AA.

AC P38005;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Unknown protein from 2D-page from elementary body (Fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE.

RC STRAIN=L2/434/Bu;

RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

RA Comanducci M., Christianen G., Birkelund S., Vreton E., Ratti G.,

RA Pallini V.;

RL Submitted (SEP-1994) to the SWISS-PROT data bank.

CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 4.5; ITS MW IS: 28 Kda.

DR Siena-2DPAGE; P38005; -.

FT NON_TER 5

SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8

DB 2 SG 3

RESULT 4

FARP_MONEX

ID FARP_MONEX STANDARD; PRT; 6 AA.

AC P41966;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FMRamide-like neuropeptide GNFRFP-amide.

OS Moniezia expansa (Sheep tapeworm).

OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;

OC Cyclophyllidae; Anoplocephalidae; Moniezia.

OX NCBI_TaxID=28841;

RN [1]

RP SEQUENCE.

RX MEDLINE=93312289; PubMed=8323531;

RA Maule A.G., Shaw C., Halton D.W., Thim L.;

RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from

RT the sheep tapeworm, Moniezia expansa.";

RT Blochem. Biophys. Res. Commun. 193:1054-1060(1993).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 6 6 AMIDATION.

SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 6;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FR 4

DB 4 FR 5

RESULT 5

TRPI_PSEPU

ID TRPI_PSEPU STANDARD; PRT; 6 AA.

AC P36414;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE TrpBA operon transcriptional activator (Fragment).

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PpGI C15;

RX MEDLINE=89335826; PubMed=2503057;

RA Eberly L., Crawford I.P.;

RT "DNA sequence of the tryptophan synthase genes of Pseudomonas

RT putida.";

RL Biochimie 71:521-531(1989).

CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE

CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

CC REGULATORS.

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CC EMBL; X13299; CAA31660.1; -.

DR InterPro; IPR000847; HTH_LYSR.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.

KW Tryptophan biosynthesis; Transcription regulation; Activator;

KW DNA-binding.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 2; DB 1; Length 6;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HD 6

DB 3 HD 4

RESULT 6

UN06_CLOPA

ID UN06_CLOPA STANDARD; PRT; 6 AA.

AC P81351;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Clostridium.
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
 II
 Db 4 AE 5

RESULT 7
 EI05_LITRU STANDARD; PRT; 7 AA.
 AC P82101;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella.";
 RT Litori electrica. Comparison with the skin peptides from Litoria
 rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YE 10
 II
 Db 2 YE 3

RESULT 8
 FAR1_ASCSU STANDARD; PRT; 7 AA.
 ID FAR1_ASCSU
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuroptide AFI.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AFI, a sequenced bioactive neuroptide isolated from the nematode
 Ascaris suum".
 RL Neuron 2:1465-1473(1989).
 CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTONEURONS. REDUCES THE
 CC INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CC CELLS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
 II
 Db 3 EF 4

RESULT 9
 UF03_MOUSE STANDARD; PRT; 7 AA.
 ID UF03_MOUSE
 AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDDB1B180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
 II
 Db 4 AE 5

RESULT 10
 AL17_CARMA STANDARD; PRT; 8 AA.
 ID AL17_CARMA
 AC P81820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 17.
 OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
 QY 7 SG 8
 Db 1 SG 2
 Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 11
 ALL5_CVDPO STANDARD; PRT; 8 AA.
 ID ALL5_CVDPO
 AC P82156;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 5
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;
 QY 8 GY 9
 Db 3 GY 4
 Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 12
 CPD1_ENTFA STANDARD; PRT; 8 AA.
 ID CPD1_ENTFA
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";
 RL Science 226:849-850(1984).
 CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC Pheromone.
 KW BACTERIOCIN PLASMID PPD1.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;
 QY 7 SG 8
 Db 7 SG 8
 Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 13
 GLUR_HUMAN STANDARD; PRT; 8 AA.
 ID GLUR_HUMAN
 AC P02729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urine glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72062338; PubMed=5126885;
 RA Lote C.J., Weiss J.B.;
 RT "Identification in urine of a low-molecular-weight highly polar
 RT glycopeptide containing cysteinyl-galactose.";
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
 CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYMER HAVING A
 CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
 DR PIR; A03188; XGHUEU.
 KW Glycoprotein.
 FT CARBOHYD 1 1 S-LINKED (GAL. .).
 SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;
 QY 5 HD 6
 Db 5 HD 6
 Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 14
 LCK5_LEUMA STANDARD; PRT; 8 AA.
 ID LCK5_LEUMA
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]

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RP SEQUENCE.
RC TISSUE-Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
RL myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
Db 2 SG 3

RESULT 15
PPK3_PERAM
ID PPK3_PERAM STANDARD; PRT: 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE-Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RL abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RL the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FR 4
Db 4 FR 5

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Search completed: April 21, 2003, 12:41:05
Job time : 7 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:37:02 : Search time 29.5 Seconds
(without alignments)
45.170 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFHRDSGYE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0
Total number of hits satisfying chosen parameters: 162749

Minimum DB seq length: 5
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002.*
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3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	22	Human APP derived
2	9	90.0	10	15	Human amyloid prec
3	9	90.0	10	22	Human APP derived
4	9	90.0	10	22	Human APP derived
5	8	80.0	10	22	Human APP derived
6	8	80.0	10	22	Human APP derived
7	7	70.0	8	23	N terminus of beta
8	7	70.0	10	22	Human APP derived
9	7	70.0	10	22	Human APP derived
10	6	60.0	7	22	Human APP A-beta p

11	6	60.0	7	23	AA014421	Synthetic peptide
12	6	60.0	8	19	AAW70865	Beta-amyloid pepti
13	6	60.0	10	22	AAAB46210	Human APP derived
14	6	60.0	10	22	AAAB46218	Human APP derived
15	5	50.0	5	23	ABB05182	Beta-amyloid pepti
16	5	50.0	6	19	AAW70868	Beta-amyloid pepti
17	5	50.0	6	23	AAU78501	Alpha secretase cl
18	5	50.0	10	21	AAU96712	Doubly phosphoryla
19	5	50.0	10	21	AAU96719	p-I-kappa-B-alpha
20	5	50.0	10	22	AAAB46209	Human APP derived
21	5	50.0	10	22	AAAB46219	Human APP derived
22	4	40.0	5	21	AAU51336	Sphingolipid desat
23	4	40.0	5	21	AAU69702	Beta-App alpha-sec
24	4	40.0	5	22	AAEL0667	Human APP-Sw mutan
25	4	40.0	5	22	AAE06907	Human Asp-2 beta-s
26	4	40.0	5	22	AAU06636	Peptide product of
27	4	40.0	5	22	AAU07235	Human beta-amyloid
28	4	40.0	6	14	AAAR32016	LAMP-3 lysosome ta
29	4	40.0	6	19	AAW70864	Beta-amyloid pepti
30	4	40.0	6	21	AAE06998	Epitope pattern #
31	4	40.0	6	22	AAAB47109	Epitope #1 used in
32	4	40.0	6	22	AAAB46199	Human APP A-beta 1
33	4	40.0	6	22	AAAB49095	Human amyloid beta
34	4	40.0	7	21	AAE07656	Peptide derived fr
35	4	40.0	7	21	AAE02941	Nucleotide-binding
36	4	40.0	8	18	AAW19494	Immunogen for rais
37	4	40.0	8	18	AAW19507	Immunogen for rais
38	4	40.0	8	20	AAU52751	Humanised ATR-5 H
39	4	40.0	9	21	AAU51340	Sphingolipid desat
40	4	40.0	9	22	AAU02736	CDR region of anti
41	4	40.0	9	22	AAU02741	CDR region of anti
42	4	40.0	9	23	ABR06519	Beta-secretase rel
43	4	40.0	10	11	AAK08279	Laminin receptor-b
44	4	40.0	10	13	AAAR24262	Human amyloidin pr
45	4	40.0	10	13	AAAR24260	Human amyloidin pr

ALIGNMENTS

RESULT 1
AAAB46214
ID AAB46214 standard; peptide; 10 AA.
XX AAB46214;
AC
XX
DT 04-APR-2001 (first entry)
XX Human APP derived immunogenic peptide #10.
DE
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -

XX Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRHDSGYE 10

Db 1 AEFRRHDSGYE 10

RESULT 2

AAR58928

ID AAR58928 standard; peptide; 10 AA.

XX

AC AAR58928;

XX

XX 15-APR-1995 (first entry)

XX Human amyloid precursor protein APP695 residues 597-606.

XX

XX Amyloid precursor protein; isoform APP 695; beta amyloid;

KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO9419692-A.

XX

PD 01-SEP-1994.

XX

XX 17-FEB-1994; 94WO-US01712.

XX

XX 18-FEB-1993; 93US-0019208.

XX

XX (GEO) GEN HOSPITAL CORP.

XX

XX Nishimoto I;

XX

XX WPI; 1994-294486/36.

XX

XX Identifying cpds. useful for treating or preventing Alzheimer's

PT disease - by determining whether it interferes with the

PT association of the couplone portion of amyloid precursor protein

PT to G polypeptide

XX

XX Disclosure; Page 33; 71pp; English.

XX

XX Beta amyloid is synthesised as part of a larger protein referred to

CC as amyloid precursor protein (APP), which has a number of isoforms

CC in humans, including APP695 and APP770. The amino terminal of beta

CC amyloid is generated by cleavage of a peptide bond of APP which in

CC APP695 lies between Met596 and Asp597. APP forms a complex with Go,

CC a GTP-binding protein (or "G protein") in brain. Go is made of one

CC alpha subunit and one Beta-gamma subunit. Two isoforms of Go, known

CC as Go1 (or GoA) and Go2 (or GoB) have been identified; they have

CC slight AA differences in their alpha subunits. The cDNA sequence and

CC deduced AA sequence of the alpha subunits in each of Go1 and Go2 are

CC shown in AAQ69002/R58914 and AAQ69004/R58924 respectively. The

CC cytoplasmic App695 sequence His657-Lys676 (AAR58913) possesses a

CC specific Go-activating function, and is necessary for complex

CC formation of this App with Go. AAR58928 is another peptide of

CC APP695 which corresp. to AAS 597-606.

XX

SQ Sequence 10 AA;

Query Match 90.0%; Score 9; DB 15; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00049;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRHDSGY 9

Db 2 AEFRRHDSGY 10

RESULT 3

AAB46213

ID AAB46213 standard; peptide; 10 AA.

XX

AC AAB46213;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #9.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

XX amyloid precursor protein; Alzheimer's disease.

OS Homo sapiens.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

XX 26-MAY-2000; 2000WO-US14810.

XX

XX 28-MAY-1999; 99US-0322289.

XX

XX (NEUR-) NEURALAB LTD.

XX

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX

DR WPI; 2001-032104/04.

XX

PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody -

XX

PS Disclosure; Figure 19; 143pp; English.

XX

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SQ Sequence 10 AA;

Query Match 90.0%; Score 9; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00049;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX
 DR WPI; 2001-032104/04.
 XX
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody.
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response. (c)
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 FRHDSGYE 10
 Db 1 FRHDSGYE 8
 |||||
 |||||
 RESULT 7
 AAU78518
 ID AAU78518 standard; Peptide; 8 AA.
 XX
 AC AAU78518;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE N terminus of beta amyloid.
 XX
 DE Alzheimer's disease; beta amyloid precursor protein; mouse;
 KW BACE; beta-site APP cleaving enzyme; neurotropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW BACE secretase/shedase; neurodegenerative disorder.
 XX
 OS Mus sp.
 XX
 PN WO200210354-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-CA01118.
 XX
 PR 01-AUG-2000; 2000CA-2313828.
 XX
 XX (RECL-) INST RECH CLINTIQUES MONTREAL.
 PA
 PI Seidah NG, Chretien M, Cromlish JA;
 XX
 XX WPI; 2002-280632/32.

XX
 PT Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/shedase for treatment of neurodegenerative disorder
 PT characterised by generation of Abeta protein, by preventing cleavage of
 PT enzyme
 XX
 PS Disclosure; Page 28; 64pp; English.
 XX
 CC This invention relates to a novel method for modulating activity of
 CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/shedase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable
 CC of hybridising with BACE mRNA, by using a ribozyme that targets and
 CC degrades BACE secretase mRNA, with a peptide that can interfere with
 CC binding of the enzyme with BACE or using an antibody or antagonist that
 CC can function as an inhibitor of BACE secretase activation. The methods
 CC of the invention modulate the activity of BACE secretase/shedase by
 CC preventing cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised
 CC by the generation of Abeta protein by measuring the levels of BACE
 CC C terminal cleavage products in a sample or tissue where an increase
 CC in cleavage products indicates a person at risk. The present sequence
 CC represents the N terminal of a beta amyloid protein of the.
 XX
 SQ Sequence 8 AA;
 Query Match 70.0%; Score 7; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFRHDS 7
 Db 2 AEFRHDS 8
 |||||
 |||||
 RESULT 8
 AAB46211
 ID AAB46211 standard; peptide; 10 AA.
 XX
 AC AAB46211;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #7.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 XX (NEUR-) NEURALAB LTD.
 PA
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX

Query Match 60.0%; Score 6; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRD 6
| | | | |
DB 2 AEFRRD 7

RESULT 11
AA014421
ID AA014421 standard; Peptide: 7 AA.

XX AC AA014421;
XX DT 02-MAY-2002 (first entry)
XX DE

XX Synthetic peptide of A-Beta residues 1-7 (DAEFRHD).

XX Neurodegenerative disorder; Alzheimer's disease; AD; T714I; APP; APP714;
XX amyloid precursor protein; amyloid Beta peptide; A-Beta; A-Beta40; brain;
XX A-Beta42; plaque pathology; pre-amyloid; cerebral amyloid angiopathy;
XX Dense-core plaque; CAA; senile plaque core; amyloid cascade; murine;
XX mouse; DAEFRHD; monoclonal antibody.

XX Mus sp.
XX Synthetic.

XX WO200202769-A1.

XX 10-JAN-2002.

XX 06-JUL-2001; 2001WO-EP07830.

XX 06-JUL-2000; 2000EP-0202362.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Cruts M, De Jonghe C, Kumar Singh S, Van Broeckhoven C;

XX WPI; 2002-154742/20.

XX Novel polynucleotide sequence encoding a mutant of amyloid precursor
XX protein 70, useful for screening for a molecule capable of reducing the
XX formation of beta amyloid 42 peptide

XX Disclosure; Page 21; 42pp; English.

XX The invention relates to the field of the neurodegenerative disorder of
XX Alzheimer's disease (AD). In particular, the invention provides a novel
XX mutation (T714I) identified in the amyloid precursor protein (APP),
XX APP714, which leads to a very aggressive form of AD. The mutation
XX involves the 43rd codon of the amyloid Beta peptide (A-Beta)
XX corresponding to the putative gamma 42-secretase cleavage site. The
XX novel mutation alters both A-Beta40 and A-Beta42 secretion elevating
XX the A-Beta42/A-Beta40 ratio by 10-fold in vitro. Furthermore, the main
XX amyloid plaque pathology in brains of these patients is of the diffuse
XX 'pre-amyloid' type composed primarily of N-truncated A-Beta42. Dense-
XX cored plaques although not absent, were significantly reduced. Also, the
XX usual sites in brain where A-Beta40 is predominantly deposited, for
XX instance, in vessels as cerebral amyloid angiopathy (CAA) or senile
XX plaque cores, were composed entirely of A-Beta42 form. Together, these
XX indicate that deposition of N-truncated A-Beta42 in one of the earliest
XX amyloid deposited in the brain, the diffuse plaques, is fully competent
XX of inciting AD either through the well-established 'amyloid cascade' or
XX by a yet unknown mechanism(s). This sequence represents a synthetic
XX peptide of A-Beta, residues 1-7 (DAEFRHD). This sequence was used for
XX raising a monoclonal antibody specific for the N-terminus of A-Beta40 and
XX A-Beta42 by immunising mice with the synthetic peptide.

XX Sequence 7 AA;

XX Query Match 60.0%; Score 6; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRD 6
| | | | |
DB 2 AEFRRD 7

RESULT 12
AAW70865
ID AAW70865 standard; peptide; 8 AA.

XX AC AAW70865;

XX DT 04-FEB-1999 (first entry)

XX DE Beta-amyloid peptide to create a monoclonal antibody.

XX Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
XX antibody; amyloid deposit; Alzheimer's disease.

XX Synthetic.

XX Homo sapiens.

XX WO9844955-A1.

XX 15-OCT-1998.

XX 09-APR-1998; 98WO-US06900.

XX 09-APR-1997; 97US-0041850.

XX (MCIN/) MCINNIS P A.

XX (MIND-) MINDSET LTD.

XX Chain DG;

XX WPI; 1998-594476/50.

XX Preventing or inhibiting progression of Alzheimer's Disease -
XX comprises use of recombinant DNA encoding an antibody specific for
XX the N- Or C-terminus of an amyloid-beta peptide

XX Example 1; Page 46; 58pp; English.

XX The present sequence represents a peptide derived from beta-amyloid
XX precursor protein (beta-APP, see AAW70863). The peptide is a
XX beta-amyloid peptide and is used to produce a monoclonal antibody
XX designated antisenilin N1/7. The specification describes a method for
XX prevention or inhibition of progression of Alzheimer's disease. The
XX method comprises administering a composition comprising a recombinant DNA
XX molecule containing a gene encoding a recombinant antibody end-specific
XX for the N-terminus or the C-terminus of an amyloid-beta peptide, operably
XX linked to a promoter which is expressed in the central nervous system.
XX The recombinant antibody molecules prevent the accumulation of
XX beta-amyloid peptides in the extracellular space, interstitial fluid and
XX cerebrospinal fluid and the aggregation of such peptides into amyloid
XX deposits in the brain. They also inhibit the progression of Alzheimer's
XX disease by inhibiting the interaction of beta-amyloid peptides mediating
XX Alzheimer's disease induced neurotoxicity and inhibiting the Alzheimer's
XX disease induced complement activation and cytokine release involved in
XX the inflammatory process.

XX Sequence 8 AA;

XX Query Match 60.0%; Score 6; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRRD 6
| | | | |
DB 2 AEFRRD 7

RESULT 13
 AAB46210
 ID AAB46210 standard; peptide; 10 AA.
 XX
 AC AAB46210;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #6.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX
 DR WPI; 2001-032104/04.
 XX
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 Query Match 60.0%; Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRD 6
 DB 5 AEFHRD 10
 |||||
 RESULT 14
 AAB46218
 ID AAB46218 standard; peptide; 10 AA.
 XX
 AC AAB46218;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #14.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX
 DR WPI; 2001-032104/04.
 XX
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
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 CC disease associated with amyloid deposits of amyloid precursor protein
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 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 Query Match 60.0%; Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 HDGSGYE 10
 DB 1 HDGSGYE 6
 |||||
 RESULT 15
 ABB05182
 ID ABB05182 standard; peptide; 5 AA.
 XX
 AC ABB05182;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Beta amyloid peptide related peptide PPI-339 SEQ ID NO:36.
 XX
 KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
 KW App-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US6319498-B1.
 XX

PD 20-NOV-2001.
XX
XX 14-MAR-1996; 96US-0617267.
XX
XX 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A, Kasman L;
PI Musso G, Signer ER, Wakefield J, Reed MJ;
XX
XX WPI; 2002-146668/19.
DR
XX
XX Anyloid modulator compound useful for treatment of an amyloidogenic
PT disease such as Alzheimer's disease comprises an aggregation core
PT domain and a modifying group attached to it -
XX
XX Example 11; Column 63; 54pp; English.
PS
XX
XX The present invention describes an amyloid modulator compound (I)
CC comprising an aggregation core domain and a modifying group attached to
CC it. (I) has nootropic, neuroprotective, immunosuppressive, antimicrobial,
CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
CC and auditory activities, and can be used as a natural amyloid aggregation
CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
CC (beta-AP). (I) are used in the manufacture of a medicament for the
CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
CC disease and other clinical occurrences of beta amyloid deposition such as
CC Down's syndrome individuals and in patients with hereditary cerebral
CC haemorrhage with amyloidosis, and for treating a disorder associated with
CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the
CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
CC not only reduces the formation of neurotoxic aggregates but also have the
CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 5 AA;
Query Match 50.0%; Score 5; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 HDSGY 9
Db 1 HDSGY 5
|||||

Search completed: April 21, 2003, 12:40:44
Job time : 29.5 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:43 ; Search time 23.5 seconds
(without alignments)
87.680 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 10
Sequence: 1 VKMDAEFRHD 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1223

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database: SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	9	P72149	pseudomonas
2	3	30.0	10	Q9J1G8	Q9J1G8 tt virus. o
3	2	20.0	7	Q47477	Q47477 escherichia
4	2	20.0	7	Q15897	Q15897 homo sapien
5	2	20.0	7	Q28742	Q28742 cryptotolagus
6	2	20.0	7	Q98866	Q98866 spinacia ol
7	2	20.0	7	O55184	O55184 rattus norv
8	2	20.0	7	Q9YVE3	Q9YVE3 human adeno
9	2	20.0	7	Q9YIR0	Q9YIR0 human adeno
10	2	20.0	7	Q9YIQ9	Q9YIQ9 human adeno
11	2	20.0	8	O68485	O68485 klebsiella
12	2	20.0	8	Q9S6D5	Q9S6D5 escherichia
13	2	20.0	8	P72221	P72221 pseudomonas
14	2	20.0	8	Q9R7T2	Q9R7T2 escherichia
15	2	20.0	8	P83158	P83158 anabaena sp
16	2	20.0	8	P83152	P83152 anabaena sp

17	2	20.0	8	2	Q9R3X0	Q9R3X0 planktothri
18	2	20.0	8	2	Q9R5L7	Q9R5L7 clostridium
19	2	20.0	8	3	Q05403	Q05403 saccharomyc
20	2	20.0	8	3	Q9URB9	Q9URB9 saccharomyc
21	2	20.0	8	4	Q15901	Q15901 homo sapien
22	2	20.0	8	4	Q9Y4J4	Q9Y4J4 homo sapien
23	2	20.0	8	4	O60773	O60773 homo sapien
24	2	20.0	8	5	Q9UB13	Q9UB13 albinaria h
25	2	20.0	8	5	P82686	P82686 periplaneta
26	2	20.0	8	6	Q9GMH3	Q9GMH3 lagenerhync
27	2	20.0	8	6	Q28866	Q28866 megaptera n
28	2	20.0	8	6	O8WNS1	O8WNS1 bos taurus
29	2	20.0	8	6	Q9TRX8	Q9TRX8 bos taurus
30	2	20.0	8	6	Q9BFC3	Q9BFC3 didelphis m
31	2	20.0	8	6	Q9BFC2	Q9BFC2 didelphis m
32	2	20.0	8	6	Q9BFC1	Q9BFC1 macropus eu
33	2	20.0	8	6	Q9BFC0	Q9BFC1 choleopus h
34	2	20.0	8	6	Q9BFB9	Q9BFC0 choleopus d
35	2	20.0	8	6	Q9BFB8	Q9BFB9 euphractus
36	2	20.0	8	6	Q9BFB7	Q9BFB8 chaetophrac
37	2	20.0	8	6	Q9BFB6	Q9BFB7 tamandua te
38	2	20.0	8	6	Q9BFB5	Q9BFB6 myrmecophag
39	2	20.0	8	6	Q9BFB4	Q9BFB5 erinaceus c
40	2	20.0	8	6	Q9BFB3	Q9BFB4 talpa altai
41	2	20.0	8	6	Q9BFB2	Q9BFB3 condylura c
42	2	20.0	8	6	Q9BFB1	Q9BFB2 sorex arane
43	2	20.0	8	6	Q9BFB0	Q9BFB1 echinops te
44	2	20.0	8	6	Q9BFA9	Q9BFB0 trichechus
45	2	20.0	8	6	Q9BFA8	Q9BFA9 procavia ca
						Q9BFA8 loxodonta a

ALIGNMENTS

RESULT 1

P72149 ID P72149 PRELIMINARY; PRT; 9 AA.
AC P72149;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative glucokinase (Fragment).
GN GLK.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-PA01.
RX MEDLINE=96427344; PubMed=8830708;
RA Sage A.E., Proctor W.D., Phibbs P.V.Jr.;
RT "A two-component response regulator, gltr, is required for glucose transport activity in Pseudomonas aeruginosa PA01.";
RL J. Bacteriol. 178:6064-6066(1996).
DR EMBL: U50932; AAC44474.1; -;
KW Kinase.
FT NON_TER
SQ SEQUENCE 9 AA; 944 MW; C3071DDAA72DC6C6 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DAE 6
|||
Db 6 DAE 8

RESULT 2

Q9J1G8 ID Q9J1G8 PRELIMINARY; PRT; 10 AA.
AC Q9J1G8;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B599CB CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AEF 7
DB 2 AEF 4

RESULT 3
Q47477 ID Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase."
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
DB 1 AE 2

RESULT 4
Q15897 ID Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (clone XP6ALLA) (Fragment).
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 20.0%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
DB 5 AE 6

RESULT 5
Q28742 ID Q28742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 20.0%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KM 3
DB 2 KM 3

RESULT 6
Q98866 ID Q98866 PRELIMINARY; PRT; 7 AA.
AC Q98866;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=86120353; PubMed=3003688;
RA  "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT  protein S11 and RNA polymerase alpha-subunit.";
RL  Nucleic Acids Res. 14:1029-1044(1986).
DR  EMBL; X03496; CAA27215.1; -.
KW  Chloroplast.
FT  NON_TER
SQ  SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match      20.0%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 FR 8
    ||
DB  2 FR 3

RESULT 7
ID  O55184      PRELIMINARY;      PRT;      7 AA.
AC  O55184;
DT  01-JUN-1998 (TrEMBLrel. 06, Created)
DR  01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GN  Orphan receptor TR4-NS (Fragment).
GS  TR4.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN  NCBI_TaxID=10116;
[1]
RP  SEQUENCE FROM N.A.
RX  STRAIN-SPRAGUE-DAWLEY;
RA  MEDLINE=96198747; PubMed=8612486;
RT  Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA  Detera-Wadleigh S.D.;
RT  "Splice variants of rat TR4 orphan receptor: differential expression
RT  of novel sequences in the 5'-untranslated region and C-terminal
RT  domain.";
RL  Endocrinology 137:1562-1571(1996).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN-SPRAGUE-DAWLEY;
RX  MEDLINE=96299786; PubMed=8661150;
RA  Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT  "New variants of the human and rat nuclear hormone receptor, TR4:
RT  expression and chromosomal localization of the human gene.";
RL  Genomics 35:361-365(1996).
DR  EMBL; U59454; AAB91433.1; -.
KW  Receptor.
FT  NON_TER
SQ  SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match      20.0%; Score 2; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 DA 5
    ||
DB  6 DA 7

RESULT 8
Q9YVE3
ID  Q9YVE3      PRELIMINARY;      PRT;      7 AA.
AC  Q9YVE3;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DR  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE  PVI core protein (Fragment).
GN  PVI.
OS  Human adenovirus type 7.
OC  Viruses; GSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX  NCBI_TaxID=10519;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-GOMEN;
RX  MEDLINE=99175282; PubMed=10074533;
RA  Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT  "Strain variation in adenovirus serotypes 4 and 7a causing acute
RT  respiratory disease.";
RL  J. Clin. Microbiol. 37:1107-1112(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-GOMEN;
RX  Crawford-Miksza L.K.;
RA  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF065065; AAD03662.1; -.
FT  NON_TER
SQ  SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match      20.0%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VK 2
    ||
DB  1 VK 2

RESULT 9
Q9YI00
ID  Q9YI00      PRELIMINARY;      PRT;      7 AA.
AC  Q9YI00;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DR  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE  01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
GN  PVI core protein (Fragment).
OS  PVI.
OC  Human adenovirus type 7a.
OX  Viruses; GSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
RN  NCBI_TaxID=85755;
[1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-KN T96-0620, S-1058, AND CL 68578;
RA  Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT  "Molecular surveillance of strain variation in adenoviruses causing
RT  acute respiratory disease, AV 4 and AV 7a.";
RL  Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF065068; AAD03668.1; -.
DR  EMBL; AF065066; AAD03664.1; -.
DR  EMBL; AF065067; AAD03666.1; -.
FT  NON_TER
SQ  SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match      20.0%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VK 2
    ||
DB  1 VK 2

RESULT 10
Q9YI09
ID  Q9YI09      PRELIMINARY;      PRT;      7 AA.
AC  Q9YI09;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DR  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE  01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
GN  PVI core protein (Fragment).

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```
GN PVI.
OS Human adenovirus type 4.
OC Viruses; GSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2-G 95-873, RI-67, AND 55142;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -
DR EMBL; AF065062; AAD03653.1; -
DR EMBL; AF065063; AAD03656.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 20.0%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2
   ||
Db 1 VK 2

RESULT 11
O68485 PRELIMINARY; PRT; 8 AA.
ID O68485;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
GN AADAL.
OS Klebsiella pneumoniae.
OG Plasmid pLQ1000.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98287600; PubMed=9624504;
RA Centron D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene aac(6')-Iq from the integron of a natural multiresistance plasmid.";
RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
DR EMBL; AF047556; AAC25501.1; -
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
   ||
Db 3 AE 4

RESULT 12
Q9S6D5 PRELIMINARY; PRT; 8 AA.
ID Q9S6D5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Putative IS30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
```

```
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Rahn A., Drummelsmith J., Whitfield C.;
RT "Conserved organization in the cps gene clusters for expression of Escherichia coli group 1 K antigens: relationship to the colanic acid biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DCLA9D1B41406 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
   ||
Db 7 AE 8

RESULT 13
P72221 PRELIMINARY; PRT; 8 AA.
ID P72221;
AC P72221;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Alginatase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RX MEDLINE=93329366; PubMed=8336113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Cloning, sequence analysis and expression in Escherichia coli of a gene encoding an alginatase lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38469; BAA21704.1; -
KW Lyase.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
   ||
Db 7 AE 8

RESULT 14
Q9R7T2 PRELIMINARY; PRT; 8 AA.
ID Q9R7T2;
AC Q9R7T2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN YQFG.
OS Escherichia coli.
```

```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996);
DR EMBL; D90705; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
Db 5 AE 6

RESULT 15
P83158
ID P83158 PRELIMINARY; PRT; 8 AA.
AC P83158;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa
DE polypeptide) (PSI-C) (Fragment).
OS Anabaena sp. (strain L31)
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
CC -!- PHOTOSYSTEM I COMPLEX.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
DR InterPro: IPR001450; 4Fe4S ferredoxin.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; PARTIAL.
KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
FT NON_TER 8
SQ SEQUENCE 8 AA; 962 MW; C5BB505322D1A1F5 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2
Db 4 VK 5

Search completed: April 21, 2003, 12:41:58
Job time : 24.5 secs

```


GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:02 ; Search time 7 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 10
Sequence: 1 VKMDAEFRHD 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	2	20.0	5	1	RE21_LITRU	P82071 litoria rub
2	2	20.0	5	1	RE31_LITRU	P82072 litoria rub
3	2	20.0	6	1	FARP_MONEX	P41966 moniezia ex
4	2	20.0	6	1	TRPI_PSEFU	P36414 pseudomonas
5	2	20.0	6	1	UN06_CLOPA	P81351 clostridium
6	2	20.0	7	1	ALL7_CYPDO	P82158 cydia pomon
7	2	20.0	7	1	FAR1_ASCSU	P31869 ascaris suu
8	2	20.0	7	1	UF03_MOUSE	P38641 mus musculu
9	2	20.0	8	1	CKKN_MACEU	P30369 macropus eu
10	2	20.0	8	1	GLUR_HUMAN	P02729 homo sapien
11	2	20.0	8	1	LCK4_LEUMA	P21143 leucophaea
12	2	20.0	8	1	ARMY_ORCLI	P82455 orconectes
13	2	20.0	8	1	PEK3_PERAM	P82618 periplaneta
14	2	20.0	8	1	UC26_MAIZE	P80632 zea mays (m
15	2	20.0	9	1	COXE_THUOB	P80975 thunus obe
16	2	20.0	9	1	DISP_RABIT	P01158 oryctolagus
17	2	20.0	9	1	FIBB_PAPAN	P19344 papio anubi
18	2	20.0	9	1	IPYR_RHOVI	P82992 rhodopsu
19	2	20.0	9	1	NEUJ_CAVPO	P34966 cavia porce
20	2	20.0	9	1	NEUX_HUMAN	P04277 homo sapien
21	2	20.0	9	1	OXYT_OCTIVU	P80027 octopus vul
22	2	20.0	9	1	ULAD_HUMAN	P31929 homo sapien
23	2	20.0	9	1	XYLA_STRSQ	P19149 streptomyc
24	2	20.0	10	1	CAER_LITXA	P56264 litoria xan
25	2	20.0	10	1	COXO_THUOB	P80982 thunus obe
26	2	20.0	10	1	FARP_MYTED	P42560 mytilus edu
27	2	20.0	10	1	FIBB_CERSI	P14537 ceratotheri
28	2	20.0	10	1	GLEM_HUMAN	P02728 homo sapien
29	2	20.0	10	1	GON3_PETMA	P30948 petromyzon
30	2	20.0	10	1	MALE_KLEPN	Q05564 klebsiella
31	2	20.0	10	1	PNEU_HUMAN	P22103 homo sapien
32	2	20.0	10	1	PNEU_RAT	P21996 rattus norv
33	2	20.0	10	1	Q2OG_COMTE	P80466 comamonas t

34	2	20.0	10	1	RRPL_PHODV	P35946 phocine dis
35	2	20.0	10	1	TKNK_PIG	P01292 sus scrofa
36	2	20.0	10	1	UPA9_HUMAN	P30095 homo sapien
37	1	10.0	5	1	ALL4_CARMA	P81817 carcinus ma
38	1	10.0	5	1	BIOA_CITFR	P13071 citrobacter
39	1	10.0	5	1	BIOB_CITFR	P12997 citrobacter
40	1	10.0	5	1	BPP7_BOTIN	P30425 bothrops in
41	1	10.0	5	1	EIO3_LITRU	P82099 litoria rub
42	1	10.0	5	1	EIO4_LITRU	P82100 litoria rub
43	1	10.0	5	1	FARP_ARTTR	P41853 artiposthi
44	1	10.0	5	1	PAP2_PARMA	P81864 pardachirus
45	1	10.0	5	1	PRCT_PERAM	P01373 periplaneta

ALIGNMENTS

RESULT 1
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 2.1
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.';
RT Aust. J. Chem. 49:955-963(1996).
RL -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 EF 7
Db 2 EF 3
RESULT 2
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog
RT 'Iltoria rubella', the skin peptide profile as a probe for the study
RL of evolutionary trends of amphibians.";

CC Aust., J. Chem. 49:955-963(1996).

CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC

CC ACTIVITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAV.

CC Amphibian skin; Amidation.

FT MOD_RES 5 5 AMIDATION.

SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EF 7

DB 2 EF 3

RESULT 3

FARP_MONEX

ID FARP_MONEX STANDARD; PRT; 6 AA.

AC F41966;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FMRFamide-like neuropeptide GNFRF-amide.

OS Montezia expansa (Sheep tapeworm).

OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;

OC Cyclophyllidae; Anoplocephalidae; Moniezia.

ON NCBI_TaxID=28841;

RN [1]

RP SEQUENCE

RX MEDLINE=93312289; PubMed=8323531;

RA Maule A.G., Shaw C., Halton D.W., Thim L.;

RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from

RT the sheep tapeworm, Montezia expansa.";

RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY

KW Neuropeptide; Amidation.

FT MOD_RES 6 6 AMIDATION.

SQ SEQUENCE 6 AA; 787 MW; 69DA09C9C4481000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FR 8

DB 4 FR 5

RESULT 4

TRPI_PSEPU

ID TRPI_PSEPU STANDARD; PRT; 6 AA.

AC P36414;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE TrpBA operon transcriptional activator (Fragment).

GN TRPI.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PPG1 C15;

RX MEDLINE=89335826; PubMed=2503057;

RA Eberly L., Crawford I.P.;

RT "DNA sequence of the tryptophan synthase genes of Pseudomonas

RT putida.";

RL Biochimie 71:521-531(1989).

CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE

CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

CC REGULATORS.

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CC -----

DR EMBL; X13299; CAA31660.1;

DR InterPro; IPR000847; HTH_LYSR.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.

KW Tryptophan biosynthesis; Transcription regulation; Activator;

KW DNA-binding.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HD 10

DB 3 HD 4

RESULT 5

UN06_CLOPA

ID UN06_CLOPA STANDARD; PRT; 6 AA.

AC P81351;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Unknown protein CP 6 from 2D-page (Fragment).

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=WS;

RX MEDLINE=98291870; PubMed=9629918;

RA Flengsgrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal

RT sequence analysis of proteins from Clostridium pasteurianum WS.";

RL Electrophoresis 19:802-806(1998).

CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6

DB 4 AE 5

RESULT 6

ALL7_CVDPO

ID ALL7_CVDPO STANDARD; PRT; 7 AA.

AC P82158;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 7
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KM 3
 ||
 DB 1 KM 2

RESULT 7
 FARL_ASCSU
 ID FARL_ASCSU STANDARD; PRT; 7 AA.
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuroptide AFL.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AFL, a sequenced bioactive neuroptide isolated from the nematode
 AS caris suum.";
 RL Neuron 2:1465-1473(1989).
 CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTONEURONS. REDUCES THE
 INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CELLS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARF (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CBI44350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EF 7
 ||
 DB 3 EF 4

RESULT 8
 UF03_MOUSE
 ID UF03_MOUSE STANDARD; PRT; 7 AA.

AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=75231108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDDB1B1180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
 ||
 DB 4 AE 5

RESULT 9
 CCKN_MACEU
 ID CCKN_MACEU STANDARD; PRT; 8 AA.
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Cholecystokinin (CCK).
 GN CCK.
 OS Macropus eugenii (Tamar wallaby), and
 OS Dasyurus viverrinus (Southeastern quoll).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315, 9279;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88234141; PubMed=3375140;
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
 RT "Cholecystokinin octapeptide purified from brains of Australian
 marsupials.";
 RL Peptides 9:429-431(1988).
 CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
 AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
 IN THE BRAIN IS NOT CLEAR.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR; A43001; A43001.
 DR PIR; PQ0012; PQ0012.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Amidation; Sulfation; Hormone.
 FT MOD_RES 2
 FT MOD_RES 8 8 SULFATION.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MD 4
 ||
 DB 6 MD 7

RESULT 10

GLUR_HUMAN STANDARD; PRT; 8 AA.

AC P02729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urine glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72062338; PubMed=5126885;
 RA Lote C.J., Weiss J.B.;
 RT "Identification in urine of a low-molecular-weight highly polar
 RT glycopeptide containing cysteinyl-galactose.";
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
 CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 CC ATTRIBUTED. AN ERTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
 CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
 DR PIR; A03188; XGHUO.
 KW Glycoprotein.
 FT CARBOHYD 1 1 S-LINKED (GAL. . .).
 SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HD 10

DB 5 HD 6

RESULT 11

LCK4_LEDMA STANDARD; PRT; 8 AA.

AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin IV (I-IV).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 AMIDATION
 SQ SEQUENCE 8 AA; 906 MW; DC63G5B1E9D5BDDA CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5

DB 1

DB 1 DA 2

RESULT 12

ORMY_ORCLI STANDARD; PRT; 8 AA.

AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orcomyotropin (OMT)
 OS Orconectes limosus (Spinycheek crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Astacidea; Astacoidea; Cambaridae; Orconectes.
 OX NCBI_TaxID=28379;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Hindgut;
 RX MEDLINE=20411310; PubMed=10952880;
 RA Dirksen H., Burdick S., Sauter A., Keller R.;
 RT "Two orckonins and the novel octapeptide orcomyotropin in the hindgut
 RT of the crayfish Orconectes limosus: identified myostimulatory
 RT neuropeptides originating together in neurones of the terminal
 RT abdominal ganglion.";
 RL J. Exp. Biol. 203:2807-2818(2000).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5

DB 2 DA 3

RESULT 13

IPK3_PERAM STANDARD; PRT; 8 AA.

AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).


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CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FR 8
Db 4 FR 5

RESULT 14
UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
Db 1 AE 2

RESULT 15
COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,

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RA Kadenbach B.;
RT "the subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EF 7
Db 5 EF 6

```

Search completed: April 21, 2003, 12:41:05
Job time : 8 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:13 ; Search time 13 Seconds
(without alignments)
73.950 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 10
Sequence: 1 VKMDAEFRHD 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1014

Minimum DB seq length: 5
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR_73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	7	2 PT0283	Ig heavy chain CRD
2	3	30.0	9	2 PL0139	carbon-monoxide de
3	2	20.0	5	2 A32516	cholecystokinin-5
4	2	20.0	5	2 C23751	spinal cord peptid
5	2	20.0	5	2 B41225	copper resistance
6	2	20.0	5	2 B31836	20K protein - Rick
7	2	20.0	5	2 PQ0009	angiotensin-conver
8	2	20.0	5	2 B37988	acid proteinase li
9	2	20.0	5	2 A44592	fulicin - giant Af
10	2	20.0	5	2 PT0596	T-cell receptor be
11	2	20.0	5	2 PT0538	T-cell receptor be
12	2	20.0	6	2 S02617	alcohol dehydrogen
13	2	20.0	6	2 S11024	hydrogensulfite re
14	2	20.0	6	2 A46474	Pc epsilon RIIB -
15	2	20.0	6	2 PT0616	T-cell receptor be
16	2	20.0	6	2 PT0687	T-cell receptor be
17	2	20.0	6	2 PT0650	T-cell receptor be
18	2	20.0	6	2 PT0550	T-cell receptor be
19	2	20.0	6	2 PT0587	T-cell receptor be
20	2	20.0	6	2 PT0568	T-cell receptor be
21	2	20.0	6	2 PT0693	T-cell receptor be
22	2	20.0	6	2 A43129	neuropeptide GNFR
23	2	20.0	7	2 B35890	RNA-directed DNA p
24	2	20.0	7	2 B39127	phosphotransferase
25	2	20.0	7	2 I46868	alpha-myosin heavy
26	2	20.0	7	2 PT0524	T-cell receptor be
27	2	20.0	7	2 PT0521	T-cell receptor be
28	2	20.0	7	2 PT0666	T-cell receptor be
29	2	20.0	7	2 PT0655	T-cell receptor be

30	2	20.0	7	2 PT0665	T-cell receptor be
31	2	20.0	7	2 PT0544	T-cell receptor be
32	2	20.0	7	2 PT0567	T-cell receptor be
33	2	20.0	7	2 PT0688	T-cell receptor be
34	2	20.0	7	2 PT0683	T-cell receptor be
35	2	20.0	7	2 PT0569	T-cell receptor be
36	2	20.0	7	2 PC2370	probable H ⁺ -transp
37	2	20.0	8	2 PQ0012	cholecystokinin -
38	2	20.0	8	2 A43001	cholecystokinin -
39	2	20.0	8	2 XGHUEU	urine glycopeptide
40	2	20.0	8	2 PC4131	hypothetical prote
41	2	20.0	8	2 S63493	dissimilatory sulf
42	2	20.0	8	2 S21273	cellulase (EC 3.2.
43	2	20.0	8	2 S21288	lectin - potato (f
44	2	20.0	8	2 PQ0726	unidentified 4.5/4
45	2	20.0	8	2 A41117	acetylcholinestera

ALIGNMENTS

RESULT 1

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DAE 6

Db 1 DAE 3

RESULT 2

PL0139
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava
C:Species: Pseudomonas carboxydoflava
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0139
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot
A:Reference number: PL0138; MUID:90055678; PMID:2818128
A:Accession: PL0139
A:Molecule type: protein
A:Residues: 1-9 <KRA>
A:Note: 2-Met is also found
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,
C:Keywords: oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DAE 6

Db 7 DAE 9

RESULT 3

A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestine
A:Reference number: A32516; MUID:87153871; PMID:3826354
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SHI>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MD 4
II
DB 3 MD 4

RESULT 4
C23751
spinal cord peptide SCP-6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C:Accession: C23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: C23751
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <HSI>
C:Superfamily: unassigned animal peptides

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5
II
DB 1 DA 2

RESULT 5
B41225
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: B41225
R:Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane proteins
A:Reference number: A41225; MUID:92020961; PMID:1924351
A:Accession: B41225
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
II
DB 1 AE 2

RESULT 6

B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A:Reference number: A31885; MUID:89008059; PMID:3139629
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 1-5 <AND>
A:Cross-references: GB:J03371; NID:gl52455; PIDN:AAD15030.1; PID:g4262874

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MD 4

II

DB 1 MD 2

RESULT 7

PQ0009
angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N:Alternate names: ficus latex peptide 2
C:Species: Ficus carica (common fig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C:Accession: PQ0009
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0009
A:Molecule type: protein
A:Residues: 1-5 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2

II

DB 4 VK 5

RESULT 8

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Ino, S.; Takeuchi, T.; Kitagaki, J.
J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase f
A:Reference number: A37988; MUID:91060608; PMID:2246266
A:Accession: B37988
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6

II

Db 1 AE 2

RESULT 9

A4692
fulicin - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C:Accession: A44692
R:Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A:Reference number: A44692; MUID:91315471; PMID:1859408
C:Accession: A44692
A:Molecule type: protein
A:Residues: 1-5 <OHT>
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F:2/Modified site: D-asparagine (Asn) #status experimental
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EF 7
||
Db 3 EF 4

RESULT 10

PT0596
T-cell receptor beta chain V-D-J region (100-2AE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0596; PT0614
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0596
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AE
A:Accession: PT0614
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1H
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5
||
Db 4 DA 5

RESULT 11

PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0538; PT0539; PT0603
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0538
A:Status: translation not shown
A:Molecule type: mRNA

A:Residues: 1-5 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A:Accession: PT0539
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A:Accession: PT0603
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5
||
Db 4 DA 5

RESULT 12

S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
C:Accession: S02617
R:Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joern
FEBS Lett. 222, 99-103, 1987
A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differ
A:Reference number: S02617; MUID:88005160; PMID:3653405
A:Accession: S02617
A:Molecule type: protein
A:Residues: 1-6 <FAI>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AE 6
||
Db 2 AE 3

RESULT 13

S11024
hydrogensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragmen
N:Alternate names: bisulfite reductase; desulfosulfidn
C:Species: Desulfovibrio thermophilus
C:Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C:Accession: S11024
R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.
Biochim. Biophys. Acta 1040, 112-118, 1990
A:Title: Purification and characterization of bisulfite reductase (desulfosulfidn) f
A:Reference number: S11024; MUID:90335276; PMID:2165817
A:Accession: S11024
A:Molecule type: protein
A:Residues: 1-6 <FAU>
C:Keywords: oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2
||
Db 3 VK 4

RESULT 14

A46474
Fc epsilon RIib - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: A46474
R:Richards, M.L.; Katz, D.H.; Liu, F.T.
J. Immunol. 147, 1067-1074, 1991
A:Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demon
A:Reference number: A46474; MUID:91318149; PMID:1861070
A:Accession: A46474
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-6 <RIC>
A:Experimental source: BALB C, splenic B cells
A>Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MD 4
||
Db 1 MD 2

RESULT 15

PT0616
T-cell receptor beta chain V-D-J region (120-1G) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0616
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0616
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5
||
Db 4 DA 5

Search completed: April 21, 2003, 12:42:30
Job time : 13 secs

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2003, 12:40:48 ; Search time 11.5 Seconds

(without alignments)
65.751 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 10

Sequence: 1 VKMDAEFRHD 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 7561385 residues

Word size : 0

Total number of hits satisfying chosen parameters: 31376

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Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	8	80.0	10	10	US-09-794-927-72
3	8	80.0	10	10	US-09-795-847-64
4	8	80.0	10	10	US-09-794-743-64
5	8	80.0	10	10	US-09-794-748-64
6	8	80.0	10	10	US-09-796-264-4
7	8	80.0	10	10	US-09-794-925-64
8	8	80.0	10	10	US-09-681-442-64
9	8	80.0	10	10	US-09-845-226-4
10	7	70.0	7	9	US-10-057-505-10
11	7	70.0	7	10	US-09-867-847-5
12	7	70.0	8	10	US-09-794-927-67
13	7	70.0	8	10	US-09-795-847-67
14	7	70.0	8	10	US-09-794-743-67
15	7	70.0	8	10	US-09-794-748-67
16	7	70.0	8	10	US-09-794-925-67
17	7	70.0	8	10	US-09-681-442-67
18	7	70.0	9	12	US-10-016-717-6
19	7	70.0	10	9	US-09-865-294-63

20	5	50.0	5	10	US-09-794-927-72	Sequence 72, Appl
21	5	50.0	5	10	US-09-795-847-72	Sequence 72, Appl
22	5	50.0	5	10	US-09-794-743-72	Sequence 72, Appl
23	5	50.0	5	10	US-09-794-748-72	Sequence 72, Appl
24	5	50.0	5	10	US-09-794-925-72	Sequence 72, Appl
25	5	50.0	5	10	US-09-681-442-72	Sequence 10, Appl
26	5	50.0	8	10	US-09-149-718-10	Sequence 5, Appl
27	5	50.0	10	9	US-09-795-903A-5	Sequence 63, Appl
28	5	50.0	10	10	US-09-794-927-63	Sequence 63, Appl
29	5	50.0	10	10	US-09-795-847-63	Sequence 63, Appl
30	5	50.0	10	10	US-09-794-743-63	Sequence 63, Appl
31	5	50.0	10	10	US-09-794-748-63	Sequence 5, Appl
32	5	50.0	10	10	US-09-796-264-5	Sequence 63, Appl
33	5	50.0	10	10	US-09-794-925-63	Sequence 63, Appl
34	5	50.0	10	10	US-09-681-442-63	Sequence 5, Appl
35	5	50.0	10	10	US-09-845-226-5	Sequence 7, Appl
36	4	40.0	6	10	US-09-808-037-7	Sequence 8, Appl
37	4	40.0	9	10	US-09-896-874-8	Sequence 8, Appl
38	4	40.0	9	10	US-09-896-139-8	Sequence 8, Appl
39	4	40.0	9	10	US-09-895-843-8	Sequence 15, Appl
40	3	30.0	5	9	US-10-179-046-15	Sequence 209, Appl
41	3	30.0	5	10	US-09-071-838-209	Sequence 21, Appl
42	3	30.0	6	9	US-09-727-963A-21	Sequence 72, Appl
43	3	30.0	6	9	US-10-059-749-72	Sequence 8, Appl
44	3	30.0	6	9	US-10-247-488-8	Sequence 89, Appl
45	3	30.0	6	9	US-10-091-135-89	

ALIGNMENTS

RESULT 1

US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lip, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09795, 903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604, 608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168, 060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177, 836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178, 368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210, 292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

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Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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11111111
DB 3 VKMDAEFR 10


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-64

Query Match          80.0%; Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
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Db 3 VKMDAEFR 10

RESULT 9
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4

Query Match          80.0%; Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
   |||||
Db 3 VKMDAEFR 10

RESULT 10
US-10-057-505-10
; Sequence 10, Application US/10057505
; Patent No. US20020164674A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: AURORA BIOSCIENCES CORPORATION
; APPLICANT: TS'EN, Roger
; APPLICANT: HEIM, Roger
; APPLICANT: CUBITT, Andrew
; TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
; FILE REFERENCE: REGEN1260-3
; CURRENT APPLICATION NUMBER: US/10/057,505
; CURRENT FILING DATE: 2002-01-25
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; PRIOR APPLICATION NUMBER: US 08/792,553
; PRIOR FILING DATE: 1997-01-31
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; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker moiety
US-10-057-505-10

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEF 7
   |||||
Db 1 VKMDAEF 7

RESULT 11
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; Sequence 5, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-5

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DAEFRHD 10
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Db 1 DAEFRHD 7

RESULT 12
US-09-794-927-67
; Sequence 67, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-67

Query Match 70.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEF 7
Db 2 VKMDAEF 8
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RESULT 13
US-09-795-847-67
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; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-67

Query Match 70.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VKMDAEF 7
Db 2 VKMDAEF 8
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RESULT 14
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; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-67

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEF 7
Db 2 VKMDAEF 8
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RESULT 15
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; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
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; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-67

Query Match 70.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 VKMDAEF 8

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Job time : 12 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:48 ; Search time 11.5 Seconds
(without alignments)
25.585 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 10
Sequence: 1 VKMDAEFRHD 10

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Gapop 60.0 ; Gapext 60.0

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Word size : 0

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Minimum DB seq length: 5
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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6	7	70.0	9	3	US-08-802-981-221
7	7	70.0	9	4	US-09-294-987-6
8	7	70.0	10	1	US-08-371-930-12
9	7	70.0	10	2	US-08-025-321C-1
10	7	70.0	10	5	PCT-US94-01712-12
11	5	50.0	5	1	US-08-480-498-1
12	5	50.0	5	2	US-08-422-333-7
13	5	50.0	5	2	US-08-659-984A-13
14	5	50.0	5	4	US-08-660-531-13
15	5	50.0	5	4	US-09-054-334-1
16	5	50.0	5	6	5187153-6
17	5	50.0	5	6	5220013-6
18	5	50.0	5	6	5223482-6
19	5	50.0	10	1	US-07-766-351-1
20	5	50.0	10	2	US-08-059-032-1
21	5	50.0	10	2	US-08-659-984A-19
22	5	50.0	10	4	US-08-660-531-19
23	5	50.0	10	4	US-09-548-372D-63
24	5	50.0	10	4	US-09-548-367D-63
25	5	50.0	10	5	PCT-US91-07290-1
26	4	40.0	7	1	US-08-136-743B-33
27	4	40.0	7	1	US-08-136-743B-35

28 4 40.0 7 1 US-08-136-743B-56 Sequence 56, Appl
29 4 40.0 7 3 US-09-040-216-29 Sequence 29, Appl
30 4 40.0 8 1 US-07-965-971-4 Sequence 4, Appl
31 4 40.0 8 1 US-08-143-697-4 Sequence 4, Appl
32 4 40.0 8 1 US-08-440-261-4 Sequence 4, Appl
33 4 40.0 8 1 US-08-440-423-4 Sequence 4, Appl
34 4 40.0 8 3 US-08-846-444-4 Sequence 4, Appl
35 4 40.0 8 5 PCT-US94-07043A-4 Sequence 4, Appl
36 4 40.0 9 3 US-08-802-981-219 Sequence 219, App
37 4 40.0 9 3 US-08-802-981-220 Sequence 220, App
38 4 40.0 9 3 US-08-802-981-222 Sequence 222, App
39 4 40.0 10 2 US-08-754-640-119 Sequence 119, App
40 4 40.0 10 3 US-08-973-225-119 Sequence 119, App
41 4 40.0 10 3 US-09-244-298A-119 Sequence 119, App
42 4 40.0 10 4 US-09-516-704-119 Sequence 119, App
43 4 40.0 10 4 US-09-549-090-119 Sequence 119, App
44 3 30.0 5 1 US-08-297-330-11 Sequence 11, Appl
45 3 30.0 5 2 US-08-637-759B-303 Sequence 303, App

ALIGNMENTS

RESULT 1
US-09-548-372D-64
; Sequence 64, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 80.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
| | | | | | | |
Db 3 VKMDAEFR 10

RESULT 2
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493

Db

1

VKMDAEF 7

RESULT 4

US-09-548-372D-67

; Sequence 67, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

; FILE REFERENCE: 29915/62801

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Peptide

US-09-548-372D-67

Query Match

Best Local Similarity

Matches

70.0%;

100.0%;

7;

Score 7;

DB 4;

Length 8;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

1

VKMDAEF 7

Db

2

VKMDAEF 8

RESULT 5

US-09-548-367D-67

; Sequence 67, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Peptide

US-09-548-367D-67

Query Match

Best Local Similarity

Matches

70.0%;

100.0%;

7;

Score 7;

DB 4;

Length 8;

0;

Mismatches

0;

Indels

0;

Gaps

0;

Db

1

VKMDAEF 8

Db

3

VKMDAEF 10

RESULT 3

US-08-792-553-10

; Sequence 10, Application US/08792553

; Patent No. 5981200

; GENERAL INFORMATION:

; APPLICANT: Tsien, Roger Y.

; APPLICANT: Heim, Roger

; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: California

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: 31-JAN-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lisa A. Haile, Ph.D.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2

; TELEPHONE: 619-678-5070

; TELEFAX: 619-678-5099

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-792-553-10

Query Match

Best Local Similarity

Matches

70.0%;

100.0%;

7;

Score 7;

DB 2;

Length 7;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

1

VKMDAEF 7

Db

1

VKMDAEF 7

Query Match

Best Local Similarity

Matches

70.0%;

100.0%;

7;

Score 7;

DB 4;

Length 8;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY 1 VKMDAEF 7
Db 2 VKMDAEF 8

RESULT 6
US-08-802-981-221
; Sequence 221, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-221

Query Match 70.0%; Score 7; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 VKMDAEF 7
Db 3 VKMDAEF 9

RESULT 7
US-09-294-987-6
; Sequence 6, Application US/09294987
; Patent No. 6313268
; GENERAL INFORMATION:
; APPLICANT: Hook, Vivian Y.H.
; TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE: P-AS 3515
; CURRENT APPLICATION NUMBER: US/09/294,987
; CURRENT FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: US 09/173,887
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9

; TYPE: PRT
; ORGANISM: mammalian
US-09-294-987-6

Query Match 70.0%; Score 7; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEF 7
Db 3 VKMDAEF 9

RESULT 8
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-12

Query Match 70.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DAEFRHD 10
Db 1 DAEFRHD 7

RESULT 9
US-08-025-321C-1
; Sequence 1, Application US/08025321C
; Patent No. 5849560
; GENERAL INFORMATION:
; APPLICANT: Abraham Ph.D., Carmela R.
; TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGRADATION
; TITLE OF INVENTION: OF AMYLOID BETA-PROTEIN PRECURSOR

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/025,321C
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0079571-0034
TELEPHONE: 617 248 5000
TELEFAX: 617 248 4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-025-321C-1

Query Match 70.0%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 1 VKMDAEF 7
Db 4 VKMDAEF 10

RESULT 10
PCT-US94-01712-12
Sequence 12, Application PC/TUS9401712
GENERAL INFORMATION:
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-12

Query Match 70.0%; Score 7; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 4 DAEFRHD 10
Db 1 DAEFRHD 7

RESULT 11
US-08-480-498-1
Sequence 1, Application US/08480498
Patent No. 5744346
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,498
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 015270-002200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-498-1

Query Match 50.0%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 VKMDA 5
Db 1 VKMDA 5

RESULT 12

US-08-422-333-7
; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIOS, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-7

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MDAEF 7
Db 1 MDAEF 5

RESULT 13
US-08-659-984A-13
; Sequence 13, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A

; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-659-984A-13

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDA 5
Db 1 VKMDA 5

RESULT 14
US-08-660-531-13
; Sequence 13, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-660-531-13

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDA 5
Db 1 VKMDA 5

RESULT 15

US-09-054-334-1
; Sequence 1, Application US/09054334
; Patent No. 6329163

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.
; APPLICANT: Jacobson-Croak, Kirsten L.
; APPLICANT: Sinha, Sukanto
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/054,334
; FILING DATE: 02-APR-1998
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002820US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-054-334-1

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDA 5
Db 1 VKMDA 5

Search completed: April 21, 2003, 12:43:00
Job time : 12.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:37:02 ; Search time 29.5 Seconds
(without alignments)
45.170 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 10
Sequence: 1 VKMDAEFRHD 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 162749

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	10	100.0	10	22	Human APP derived
2	9	90.0	10	22	Human APP derived
3	9	90.0	10	22	Human APP derived
4	8	80.0	10	13	Human amyloidin pr
5	8	80.0	10	21	Beta-APP alpha-sec
6	8	80.0	10	22	Human wild-type AP
7	8	80.0	10	22	Human amyloid prec
8	8	80.0	10	22	Asp2 recognition s
9	8	80.0	10	22	Human beta-amyloid
10	8	80.0	10	22	Human wild-type AP

11	8	80.0	10	22	AA66574	Synthetic peptide
12	8	80.0	10	22	AA66208	Human APP derived
13	8	80.0	10	22	AA66212	Human APP derived
14	8	80.0	10	22	AA66136	Synthetic peptide f
15	8	80.0	10	23	AAU99490	Peptide #1 used as
16	8	80.0	10	23	AB278615	Beta-secretase spe
17	8	80.0	10	23	AB278615	Human APP beta-sec
18	7	70.0	7	22	AA66202	Human APP A-beta p
19	7	70.0	7	23	AA66202	Beta-secretase pep
20	7	70.0	7	23	AA66202	Synthetic peptide
21	7	70.0	8	19	AA66202	Beta-amyloid pepti
22	7	70.0	8	21	AA66202	Beta-secretase sub
23	7	70.0	8	22	AA66202	Human Aspartyl pro
24	7	70.0	8	22	AA66202	Human amyloid prec
25	7	70.0	8	22	AA66202	Beta secretase sub
26	7	70.0	8	22	AA66202	Synthetic fluoresc
27	7	70.0	8	22	AA66202	Human beta-amyloid
28	7	70.0	8	22	AA66202	Human Aspartyl pro
29	7	70.0	8	23	AB278615	APP Swedish mutant
30	7	70.0	8	23	AB278615	N terminus of beta
31	7	70.0	9	19	AA66202	Fluorogenic protea
32	7	70.0	9	21	AA66202	A peptide fragment
33	7	70.0	9	21	AA66202	Mammalian amyloid
34	7	70.0	10	13	AA66202	Peptide Pl. Synth
35	7	70.0	10	15	AA66202	Human amyloid prec
36	7	70.0	10	15	AA66202	Human amyloid beta
37	7	70.0	10	22	AA66202	Beta-sheet breaker
38	7	70.0	10	22	AA66202	Human APP derived
39	7	70.0	10	22	AA66202	Human APP derived
40	6	60.0	6	19	AA66202	Beta-amyloid pepti
41	6	60.0	10	13	AA66202	Human amyloidin pr
42	6	60.0	10	21	AA66202	Beta-APP alpha-sec
43	6	60.0	10	21	AA66202	Beta-APP alpha-sec
44	6	60.0	10	22	AA66202	Human APP derived
45	6	60.0	10	22	AA66202	Human APP derived

ALIGNMENTS

RESULT 1
AAB46210
ID AAB46210 standard; peptide; 10 AA.
XX
AC AAB46210;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #6.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody

XX Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10

DB 1 VKMDAEFRHD 10

RESULT 2

AAB46209

ID AAB46209 standard; peptide; 10 AA.

AC AAB46209;

XX 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #5.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

OS WO200072880-A2.

PN 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14810.

PF 28-MAY-1999; 99US-0322289.

XX (NEUR-) NEURALAB LTD.

PA Schenk DB, Bard F, Vasquez NJ, Yednock T;

PI WPI; 2001-032104/04.

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PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody

XX Disclosure; Figure 19; 143pp; English.

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CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

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CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match 90.0%; Score 9; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRH 9

DB 2 VKMDAEFRH 10

RESULT 3

AAB46211

ID AAB46211 standard; peptide; 10 AA.

XX AAB46211;

XX 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #7.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

OS WO200072880-A2.

PN 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14810.

PF 28-MAY-1999; 99US-0322289.

XX (NEUR-) NEURALAB LTD.

PA Schenk DB, Bard F, Vasquez NJ, Yednock T;

PI WPI; 2001-032104/04.

DR Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody

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CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match 90.0%; Score 9; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDAEFRHD 10

```

Db      1  VKMDAEFRHD 9
|||||
RESULT 4
AAR24261
ID  AAR24261 standard; Protein; 10 AA.
AC  AAR24261;
XX
DT  09-NOV-1992 (first entry)
XX
DE  Human amyloidin protease substrate sequence #1.
XX
KW  Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW  metalloprotease; hAP; protease inhibitor; APP592-601
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  Modified-site 1
FT  /note= "Acetylated-Ser"
XX
XX  WO9207068-A.
XX  30-APR-1992.
XX
XX  04-OCT-1991; 91WO-US07290.
XX
XX  05-OCT-1990; 90US-0594122.
XX  30-SEP-1991; 91US-0766351.
XX
XX  (ATHE-) ATHENA NEUROSCIENCES INC.
XX  (ELIL) LILLY & CO ELI.
XX
XX  Dovey HF, Johnstone EM, Little SP, McConlogue L, Seubert PA;
XX  Sinha S;
XX  WPI; 1992-167148/20.
XX
XX  Human amyloidin protease - used for cleaving Met-Asp bond in
XX  amyloid-like substrate for identifying protease inhibitors
XX
XX  Claim 1; Page 52; 62pp; English.
XX
XX  Claimed human amyloidin protease is defined by its ability to
XX  cleave the Met-Asp bond of this synthetic substrate. The substrate,
XX  which corresponds to residues 592 to 601 of the 695 amino acid APP,
XX  can be used in an assay for identifying inhibitors of proteases
XX  which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase or
XX  rat mast cell protease I or II.
XX  See AAR24260-3, AAR24266-7 and AAR24875-Q24887.
XX
SQ  Sequence 10 AA;

Query Match 80.0%; Score 8; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1  VKMDAEFR 8
Db      3  VKMDAEFR 10
|||||

RESULT 5
AAY69703
ID  AAY69703 standard; peptide; 10 AA.
XX
AC  AAY69703;
XX
DT  11-APR-2000 (first entry)
XX
DE  Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).

```

```

XX
KW  Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW  cleavage site; beta-secretase; neurodegenerative disease;
KW  Alzheimer's disease.
XX
OS  Homo sapiens.
XX
PN  WO9964587-A1.
XX
PD  16-DEC-1999.
XX
XX  04-JUN-1999; 99WO-FR01326.
XX
XX  05-JUN-1998; 98FR-0007068.
XX  31-MAR-1999; 99US-0122599.
XX
XX  (RHON) RHONE-POULENC RORER SA.
XX  (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX  Rhoulam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX  WPI; 2000-097537/08.
XX
XX  Polypeptide with beta-secretase activity, specific for wild-type
XX  amyloid precursor protein, useful in treating Alzheimer's disease
XX
XX  Example 3; Page 24; 44pp; French.
XX
XX  Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
XX  novel polypeptide with beta-secretase activity that can cleave
XX  specifically the natural beta-amyloid precursor protein (BAPP). Normal
XX  cleavage of the protein occurs between amino acids Met596-Asp597 and
XX  Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
XX  polypeptide is used to identify agents that interact specifically with
XX  it. These agents regulate metabolism of APP, particularly they slow down
XX  or reduce production of beta-amyloid, so can be used to treat
XX  neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ  Sequence 10 AA;

Query Match 80.0%; Score 8; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1  VKMDAEFR 8
Db      3  VKMDAEFR 10
|||||

RESULT 6
AAEL0654
ID  AAEL0654 standard; peptide; 10 AA.
XX
XX  AAEL0654;
XX
XX  10-DEC-2001 (first entry)
XX
XX  Human wild-type APP beta-secretase peptide, PHA-95812E.
XX
XX  Human; aspartyl protease 1; Asp1; amyloid precursor protein;
XX  Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX  amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
XX  APP beta-secretase peptide.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  FH Cleavage-site 5..6
XX
XX  GB2357767-A.
XX
XX  04-JUL-2001.
XX

```


PN WO200149098-A2.
 XX 12-JUL-2001.
 PD
 XX
 PF 09-MAY-2001; 2001WO-IB00798.
 XX
 PR 09-MAY-2001; 2001WO-IB00798.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI; 2001-502549/55.
 DR
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 PS Claim 127; Page 101; 185pp; English.
 XX
 CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC APP oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is a peptide substrate
 CC for Asp2 corresponding to the wild-type APP beta-secretase site.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 Db 3 VKMDAEFR 10
 |||||
 RESULT 9
 AAU07227
 ID AAU07227 standard; Peptide; 10 AA.
 XX
 AC AAU07227;
 XX
 DT 24-OCT-2001 (first entry)
 DE Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.
 XX
 DE Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 XX

KW beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.
 XX Homo sapiens.
 OS
 XX WO200149097-A2.
 PN
 XX 12-JUL-2001.
 PD
 XX
 PF 09-MAY-2001; 2001WO-IB00797.
 XX
 PR 09-MAY-2001; 2001WO-IB00797.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI; 2001-502548/55.
 DR
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 PS Claim 127; Page 101; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP-beta40
 CC and APP-beta42 secretase sites.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 Db 3 VKMDAEFR 10
 |||||
 RESULT 10
 AA02606
 ID AA02606 standard; peptide; 10 AA.
 XX
 AC AA02606;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 XX Human wild-type APP beta-secretase substrate peptide, PHA-95812E.
 XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
 KW beta-secretase.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 XX
 PN WO200123533-A2.
 XX
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US26080.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 XX
 PS Example 12; Page 85; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human wild-type amyloid
 CC precursor protein (APP) beta-secretase specific substrate peptide,
 CC PHA-95812E. This peptide is used for assaying the beta-secretase activity
 CC of human Aspartyl protease 2a (Asp2a) protein. The peptide is also used
 CC for determining the relationship between Aspartyl protease 1 (Asp1) and
 CC APP protein.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 DB 3 VKMDAEFR 10
 |||||
 RESULT 11
 AAB66574
 ID AAB66574 standard; Peptide; 10 AA.
 XX
 AC AAB66574;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Synthetic peptide derived from APP beta-secretase site.
 XX
 KW Memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
 KW APP; memapsin 2 inhibitor; Alzheimer's disease.
 XX
 OS Synthetic.
 XX
 PN WO200100665-A2.
 XX
 PD 04-JAN-2001.
 XX

PF 27-JUN-2000; 2000WO-US17742.
 XX
 PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178388.
 PR 08-JUN-2000; 2000US-0210292.
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Tang JJN, Hong L, Ghosh AK;
 XX
 DR WPI; 2001-137933/14.
 XX
 PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
 PT having 2 catalytic aspartic residues and substrate binding cleft, used
 PT to treat Alzheimer's disease by blocking amyloid precursor protein
 PT cleavage -
 XX
 PS Disclosure; Page 11; 86pp; English.
 XX
 CC The present sequence is given in a specification relating to an inhibitor
 CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
 CC active site, which is defined by the presence of two catalytic aspartic
 CC residues and a substrate binding cleft. The inhibitor is useful for
 CC the treatment and diagnosis of Alzheimer's disease. It is useful in
 CC screens for individuals with a genetic predisposition to Alzheimer's
 CC disease. The inhibitor is useful as a reagent for specifically binding to
 CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
 CC isolation, purification and characterisation.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 DB 3 VKMDAEFR 10
 |||||
 RESULT 12
 AAB46208
 ID AAB46208 standard; peptide; 10 AA.
 XX
 AC AAB46208;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #4.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2000072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Vednock T;
 XX
 DR WPI; 2001-032104/04.
 XX

PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody

XX Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFR 8
 |||||
 Db 3 VKMDAEFR 10

RESULT 13
 AAB46212
 ID AAB46212 standard; peptide; 10 AA.
 XX
 AC AAB46212;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #8.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX WPI; 2001-032104/04.
 XX
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody

XX Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 MDAEFRHD 10
 |||||
 Db 1 MDAEFRHD 8

RESULT 14
 AAB61336
 ID AAB61336 standard; peptide; 10 AA.
 XX
 AC AAB61336;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Synthetic peptide from beta amyloid precursor protein.
 XX
 KW Memapsin 2; catalyst; Alzheimer's.
 XX
 OS Unidentified.
 XX
 PN WO200100663-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 27-JUN-2000; 2000WO-US17661.
 XX
 PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178368.
 PR 08-JUN-2000; 2000US-0210292.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Tang JJN, Lin X, Koelsch G;
 XX WPI; 2001-102885/11.
 XX
 PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease -
 XX
 PS Claim 6; Page 11; 86pp; English.
 XX
 CC The present invention relates to a purified recombinant
 CC catalytically active memapsin 2. The invention may be used for
 CC isolating inhibitors which are used to treat or prevent
 CC Alzheimer's disease. The invention may also be used to screen
 CC for individuals more genetically prone to develop Alzheimer's
 CC disease.

XX Sequence 10 AA;
 Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFR 8
 |||||
 Db 3 VKMDAEFR 10

```

RESULT 15
AAU99490
ID AAU99490 standard; peptide; 10 AA.
XX
XX AC AAU99490;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX DE Peptide #1 used as substrate for human memapsin 2.
XX
XX KW Human; memapsin 2; beta secretase; aspartic protease; APP;
XX KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
XX KW neuroprotective; nootropic.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN US2002049303-A1.
XX
XX PD 25-APR-2002.
XX
XX PF 28-FEB-2001; 2001US-0796264.
XX
XX PR 28-JUN-1999; 99US-141363P.
XX PR 30-NOV-1999; 99US-168060P.
XX PR 25-JAN-2000; 2000US-177838P.
XX PR 27-JAN-2000; 2000US-178368P.
XX PR 27-JUN-2000; 2000US-0604608.
XX
XX PA (TANG/) TANG J J N.
XX PA (LINX/) LIN X.
XX PA (KOEL/) KOELSCH G.
XX PA (HONG/) HONG L.
XX
XX PI Tang JJN, Lin X, Koelsch G, Hong L;
XX
XX DR WPI; 2002-507280/54.
XX
XX PT New recombinant catalytically active memapsin 2, useful to screen for
XX PT inhibitors of memapsin 2 which can be used to prevent and treat
XX PT Alzheimer's disease.
XX
XX PS Claim 6; Page 30; 44pp; English.
XX
XX CC The present invention relates to methods for the production of
XX CC purified, recombinant catalytically active, memapsin 2 (beta
XX CC secretase). Memapsin 2, a member of the aspartic protease family,
XX CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
XX CC The recombinant memapsin 2 is useful for identifying inhibitors of
XX CC memapsin 2 in the design of drugs for the treatment and/or prevention
XX CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
XX CC immunise against Alzheimer's disease. The present sequence represents
XX CC a peptide used as a substrate for human memapsin 2.
XX
XX SQ Sequence 10 AA;

Query Match 80.0%; Score 8; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
   | | | | |
DB 3 VKMDAEFR 10

Search completed: April 21, 2003, 12:40:44
Job time : 30.5 secs

```

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:03:55 ; Search time 28 Seconds
(without alignments)

309.071 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSNGKAIIGLMVGGVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	100.0	82	4	Q16014 homo sapien
2	217	100.0	82	4	Q16019 homo sapien
3	217	100.0	82	4	Q16020 homo sapien
4	217	100.0	82	4	P78438 homo sapien
5	217	100.0	534	13	O93296 gallus gall
6	217	100.0	569	13	O9PVL1 gallus gall
7	217	100.0	695	6	O95KN7 macaca fasc
8	217	100.0	695	11	O60496 cavia sp. p
9	217	100.0	695	13	O9DGJ8 gallus gall
10	217	100.0	751	13	O9DGJ7 gallus gall
11	217	100.0	770	6	O9TUI0 sus scrofa
12	207	95.4	97	4	Q13778 homo sapien
13	198	91.2	79	11	O35463 cricetus
14	198	91.2	607	11	O99K32 mus musculus
15	198	91.2	693	13	Q98SG0 xenopus lae
16	198	91.2	695	11	P97487 mus musculus

17	198	91.2	747	13	Q91963
18	195	89.9	695	13	Q98SF9
19	188	86.6	699	13	O57394
20	176	81.1	33	4	Q9UC33
21	175	80.6	780	13	O73683
22	171	78.8	737	13	O93279
23	162	74.7	30	4	Q9UCA9
24	157.5	72.6	357	13	Q8UUI8
25	157.5	72.6	472	13	Q8UUS0
26	157.5	72.6	612	13	Q919E7
27	157.5	72.6	738	13	Q90W28
28	156	71.9	239	13	Q8UUI7
29	156	71.9	694	13	Q8UUR9
30	147	67.7	28	4	Q9UCD1
31	121	55.8	49	6	O97917
32	106	48.8	19	4	Q9UC88
33	95	43.8	35	4	O8WZ99
34	64	29.5	328	2	O8RPS4
35	63	29.0	321	16	O8RG41
36	63	29.0	755	2	Q9R717
37	63	29.0	755	2	Q9R472
38	63	29.0	755	2	Q9R694
39	63	29.0	755	16	Q8U6A3
40	62	28.6	755	2	O44388
41	60	27.6	755	2	Q9WFA1
42	59	27.2	20	4	Q9UCB6
43	57.5	26.5	895	10	Q9AWB6
44	57	26.3	195	10	O22662
45	57	26.3	332	12	Q9DQNS

ALIGNMENTS

RESULT 1

ID	Q16014	PRELIMINARY;	PRT;	82	AA.
AC	Q16014;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Beta-amyloid peptide (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93236601; PubMed=8476439;				
RA	Denman R.B., Rosenzweig R., Miller D.L.;				
RT	"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."				
RL	Biochem. Biophys. Res. Commun. 192:96-103(1993).				
DR	EMBL; S60721; AAB26263.2; -.				
DR	HSSP; P05067; 1BA4.				
DR	InterPro; IPR001255; Beta-APP.				
DR	Pfam; PF03494; Beta-APP; 1.				
FT	NON_TER 1				
FT	NON_TER 82				
SQ	SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;				
Query Match 100.0%; Score 217; DB 4; Length 82;					
Best Local Similarity 100.0%; Pred. No. 1.9e-22;					
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 DAEFRHDSGYEVHHQKLVFFAEDVGSNGKAIIGLMVGGVIA 42				
Db	18 DAEFRHDSGYEVHHQKLVFFAEDVGSNGKAIIGLMVGGVIA 59				
RESULT 2					
Q16019					
ID	Q16019	PRELIMINARY;	PRT;	82	AA.

ID	PRELIMINARY;	82 AA.	PRT;
P78438			
AC			
DT	01-MAY-1997 (TrEMBLrel. 03, Created)		
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Amyloid protein (Beta-amyloid protein) (Fragment).		
GN	APP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
NCBI_TaxID=9606;			
11]			
RN	SEQUENCE FROM N.A.		
RP			
RX	MEDLINE=89392030; PubMed=2675837;		
RA	Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,		
RA	Little S.P.;		
RA	"Alzheimer's disease amyloid peptide is encoded by two exons and shows		
RT	similarity to soybean trypsin inhibitor."		
RL	Biochem. Biophys. Res. Commun. 163:1248-1255(1989).		
RN	[2]		
RN	SEQUENCE OF 19-48 FROM N.A.		
RX	MEDLINE=871120329; PubMed=2949367;		
RP	Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,		
RA	Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;		
RA	"Amyloid beta protein gene: cDNA, mRNA distribution, and genetic		
RT	linkage near the Alzheimer locus."		
RL	Science 235:880-884(1987).		
RN	[3]		
RN	SEQUENCE OF 32-63 FROM N.A.		
RX	MEDLINE=93035397; PubMed=1415269;		
RP	Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,		
RA	Anderson L., O'dahl S., Nemens E., White J.A.;		
RA	"Linkage and mutational analysis of familial Alzheimer disease		
RT	kinds for the APP gene region."		
RL	Am. J. Hum. Genet. 51:998-1014(1992).		
DR	EMBL; M29270; AAA51768.1; .		
DR	EMBL; M29269; AAA51768.1; JOINED.		
DR	EMBL; M15532; AAA51564.1; .		
DR	EMBL; S45136; AAB23646.1; .		
DR	HSP; P05067; IBA4.		
DR	InterPro: IPR001255; Beta-APP.		
DR	Pfam: PF03494; Beta-APP; 1.		
FT	NON_TER		
SQ	SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;		
	Query Match	100.0%;	Score 217; DB 4; Length 82;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-22;
	Matches 42; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42		
Db	17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 58		
RESULT 5			
O93296	PRELIMINARY;	PRT;	534 AA.
AC			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Amyloid protein (Fragment).		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
NCBI_TaxID=9031;			
11]			
RN	SEQUENCE FROM N.A.		
RP			
RX	MEDLINE=98337885; PubMed=9671674;		
RA	Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,		
RA	Milligan C.E.;		
RT	"Increased production of amyloid precursor protein provides a		

RT substrate for caspase-3 in dying motoneurons. ";

RL J. Neurosci. 18:5869-5880(1998).

DR EMBL; AF042098; AAC25052.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1

SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2B6604C92 CRC64;

Query Match

Best Local Similarity 100.0%; Score 217; DB 13; Length 534;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 436 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 477

RESULT 6

Q9PVL1

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.

AC Q9PVL1;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Amyloid protein (Fragment).

GN APP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;

RT "What the evolution of the amyloid protein precursor supergene family

RF tells us about its function.";

RL Neurochem. Int. 0:0-0(2000).

DR EMBL; AF030341; AAF12698.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1

SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match

Best Local Similarity 100.0%; Score 217; DB 13; Length 569;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 472 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 513

RESULT 7

Q95KN7

ID Q95KN7 PRELIMINARY; PRT; 695 AA.

AC Q95KN7;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Amyloid b-protein precursor.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopithecinidae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=CEREBELLUM;

RA MEDLINE=91273117; PubMed=1905108;

RA Podlisky M.B., Tolan D.R., Selkoe D.J.;

RT "Homology of the amyloid beta protein precursor in monkey and human

RT supports a primate model for beta amyloidosis in Alzheimer's

RT disease.";

RL Am. J. Pathol. 138:1423-1435(1991).

DR EMBL; M58727; AAA36829.1; -.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PROSITE; PS00319; A4_EXTRA; UNKNOWN_1.

DR PROSITE; PS00320; A4_INTRA; UNKNOWN_1.

DR SIGNAL 1

DR CHAIN 597 636 POTENTIAL.

SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match

Best Local Similarity 100.0%; Score 217; DB 6; Length 695;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 597 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 638

RESULT 8

Q60496

ID Q60496 PRELIMINARY; PRT; 695 AA.

AC Q60496;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Putative amyloid precursor protein.

OS Cavia sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10143;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA MEDLINE=97236426; PubMed=9116031;

RA Beck M., Mueller D., Bigl V.;

RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and

RT alternative splicing.";

RL Biochim. Biophys. Acta 1351:17-21(1997).

DR EMBL; X97631; CAA66230.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match

Best Local Similarity 100.0%; Score 217; DB 11; Length 695;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

|||||

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldhaber D., Lerman M.L., McBride O.W., Saffioti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 RL brain amyloid of Alzheimer's disease."; Science 235:877-880(1987).
 DR EMBL: M15533; AAA35540.1; -
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;
 Query Match 95.4%; Score 207; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.5e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 EFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 1 EFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40
 |||||
 RESULT 13
 O35463 PRELIMINARY; PRT; 79 AA.
 ID O35463;
 AC O35463;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN BETA APP.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030413; AAB86608.1; -
 DR HSSP: P05067; 1BA4
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 79
 SQ SEQUENCE 79 AA; 8538 MW; 372C6C3BFF3F597 CRC64;

Query Match 91.2%; Score 198; DB 11; Length 79;
 Best Local Similarity 92.9%; Pred. No. 7.6e-20;
 Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 21 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 62
 |||||
 RESULT 14
 O99K32 PRELIMINARY; PRT; 607 AA.
 ID O99K32
 AC O99K32;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 68.4 kDa protein (Fragment).
 GN APP.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005490; AA05490.1; -
 DR HSSP: P05067; 1AAP.
 DR MGD: MGI:88059; APP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Hypothetical protein; Serine protease inhibitor.
 FT NON_TER 1
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;
 Query Match 91.2%; Score 198; DB 11; Length 607;
 Best Local Similarity 92.9%; Pred. No. 8.8e-19;
 Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 509 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 550
 |||||

RESULT 15
 O98SGO PRELIMINARY; PRT; 693 AA.
 ID O98SGO
 AC O98SGO;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-amyloid precursor protein A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ298150; CAC37193.1; -
 DR HSSP: P05067; 1HZ3.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT SIGNAL
 KW SIGNAL
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF555C1AB653 CRC64;
 Query Match 91.2%; Score 198; DB 13; Length 693;
 Best Local Similarity 88.1%; Pred. No. 1e-18;
 Matches 37; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:01:04 ; Search time 11 seconds
(without alignments)
158.364 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAERFHDGSEVHHKLVFF.....DVGSNKGAILGLMVGWVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	217	100.0	57	1	A4_PIG	Q29023 sus scrofa
2	217	100.0	57	1	A4_URSM	Q29149 ursus marit
3	217	100.0	58	1	A4_CANFA	Q28280 canis famil
4	217	100.0	58	1	A4_RABIT	Q28748 oryctolagus
5	217	100.0	58	1	A4_SHEEP	Q28757 ovis aries
6	217	100.0	59	1	A4_BOVIN	Q28053 bos taurus
7	217	100.0	751	1	A4_SAISC	Q95241 salmtr sci
8	217	100.0	770	1	A4_HUMAN	P05067 homo sapien
9	198	91.2	770	1	A4_MOUSE	P12023 mus musculu
10	198	91.2	770	1	A4_RAT	P08592 rattus norv
11	62	28.6	755	1	TR2M_AGR4	P04029 agrobacteri
12	61	28.1	755	1	TR2N_AGRVI	P25017 agrobacteri
13	57	26.3	327	1	POLG_PVYCH	P21294 potato viru
14	57	26.3	503	1	Y226_MYCPN	P75462 mycoplasma
15	56.5	26.0	378	1	SLGI_YEAST	P54867 saccharomyc
16	55.5	25.6	297	1	FTR_ARCFU	Q28076 archaeoglob
17	55	25.3	488	1	DHAL_PSESP	P33008 pseudomonas
18	55	25.3	3063	1	POLG_PVYN	P18247 p genome po
19	54.5	25.1	967	1	PDB1_ARATH	P93733 arabidopsis
20	54	24.9	284	1	POLG_PVYIO	P11897 potato viru
21	53.5	24.7	708	1	YNZB_CAEEL	P45972 caenorhabdi
22	53.5	24.7	971	1	Y228_BORBU	O51246 borrelia bu
23	52	24.0	611	1	YCR3_YEAST	P25351 saccharomyc
24	51	23.5	494	1	COBQ_MYCTU	O53677 mycobacteri
25	51	23.5	769	1	ITB2_BOVIN	P32592 bos taurus
26	50.5	23.3	915	1	PDB2_ARATH	Q23078 arabidopsis
27	50	23.0	285	1	MENB_HAEIN	P44960 haemophilus
28	50	23.0	1437	1	MRP5_HUMAN	O15460 homo sapien
29	50	23.0	3579	1	STAN_DROME	Q9v5n8 drosophila
30	49.5	22.8	1162	1	VGL2_IBVM	P12651 avian infec
31	49	22.6	246	1	TPIS_CULTA	P30741 culicx tarsa
32	49	22.6	322	1	Y853_RICPR	Q9zca7 rickettsia
33	49	22.6	403	1	PGK_STRCO	Q9z519 streptomyce

34	49	22.6	432	1	PURA_RHILO	Q98f97 rhizobium l
35	49	22.6	568	1	NIRS_PSEAE	P24474 pseudomonas
36	49	22.6	674	1	TML1_ARATH	P33543 arabidopsis
37	49	22.6	704	1	SSP2_BOMMO	P20613 bombyx mori
38	49	22.6	753	1	PPE2_HUMAN	O14830 homo sapien
39	49	22.6	757	1	PPE2_MOUSE	O35385 mus musculus
40	49	22.6	1080	1	HDC_DROME	Q9nm88 drosophila
41	48.5	22.4	160	1	FMDR_ECOLI	P24093 escherichia
42	48.5	22.4	330	1	COAT_PEMV	P07993 pepper mott
43	48.5	22.4	393	1	GUN1_USTMA	P54424 ustilago ma
44	48.5	22.4	459	1	Y226_MYCGE	P47468 mycoplasma
45	48.5	22.4	497	1	GLYA_CHLPN	Q9z831 chlamydia p

ALIGNMENTS

RESULT 1
A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X561327; CAA39592.1; --
CC HSP; P05067; 1BA4.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC Pfam; PF03494; Beta-APP; 1.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neutone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC NON_TER 57 57
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 2

A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56128; CAA39593.1; -.
DR HSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 3

A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56125; CAA39590.1; -.
DR HSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 217; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 8.1e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 48

RESULT 4

A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 CC EMBL; X56129; CAA39594.1; -;
 CC HSSP; P05067; 1BA4.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC FT CHAIN 1 1
 CC FT DOMAIN 6 48 * BETA-AMYLOID PROTEIN (POTENTIAL).
 CC FT TRANSMEM 34 57
 CC FT DOMAIN 58 >58
 CC FT NON_TER 58 58
 CC FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 CC
 CC Query Match 100.0%; Score 217; DB 1; Length 58;
 CC Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 CC Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 CC |
 CC DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
 CC
 CC RESULT 5
 CC A4_SHEEP
 CC ID A4_SHEEP STANDARD; PRT; 58 AA.
 CC AC Q28757;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 CC protein (Beta-APP) (A-beta)] (Fragment).
 CC GN APP.
 CC OS Ovis aries (Sheep).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_TaxID=9940;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Heart;
 CC RX MEDLINE=9201079; PubMed=1656157;
 CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 CC "Conservation of the sequence of the Alzheimer's disease amyloid
 CC peptide in dog, polar bear and five other mammals by cross-species
 CC polymerase chain reaction analysis.";
 CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----

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 CC -----
 CC EMBL; X56130; CAA39595.1; -;
 CC HSSP; P05067; 1BA4.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC FT CHAIN 1 1
 CC FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC FT TRANSMEM 34 57
 CC FT DOMAIN 58 >58
 CC FT NON_TER 58 58
 CC FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 CC
 CC Query Match 100.0%; Score 217; DB 1; Length 58;
 CC Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 CC Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 CC |
 CC DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47
 CC
 CC RESULT 6
 CC A4_BOVIN
 CC ID A4_BOVIN STANDARD; PRT; 59 AA.
 CC AC Q28053;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 CC protein (Beta-APP) (A-beta)] (Fragment).
 CC GN APP.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=92017079; PubMed=1656157;
 CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 CC "Conservation of the sequence of the Alzheimer's disease amyloid
 CC peptide in dog, polar bear and five other mammals by cross-species
 CC polymerase chain reaction analysis.";
 CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X56124; CAA39589.1; -;
 CC DB EMBL; X56126; CAA39591.1; -;
 CC DR

HSP: P05067; 1B44.
 InterPro: IPR001868; A4_APP.
 InterPro: IPR001255; Beta-APP.
 Pfam: PF03494; Beta-APP; 1.
 PROSITE: PS00319; A4_EXTRA; PARTIAL.
 PROSITE: PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.
 NON_TER 1 1
 CHAIN 7 49
 DOMAIN <1 34
 TRANSMEM 35 58
 DOMAIN 59 >59
 NON_TER 59 59
 SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
 Query Match 100.0%; Score 217; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 8.2e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 42
 DB 7 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 48
 RESULT 7
 A4_SAISC STANDARD; PRT; 751 AA.
 ID: A4_SAISC
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RX Levy E., Anorini A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 CC EMBL: S81024; AAD14347.1; -.
 DR HSP: P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 PROSITE: PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.
 NON_TER 1 1
 CHAIN 7 49
 DOMAIN <1 34
 TRANSMEM 35 58
 DOMAIN 59 >59
 NON_TER 59 59
 SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
 Query Match 100.0%; Score 217; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 8.2e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 42
 DB 7 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 48
 RESULT 7
 A4_SAISC STANDARD; PRT; 751 AA.
 ID: A4_SAISC
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RX Levy E., Anorini A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 CC EMBL: S81024; AAD14347.1; -.
 DR HSP: P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 PROSITE: PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 NON_TER 1 17
 CHAIN 18 751
 DOMAIN 18 680
 TRANSMEM 681 704
 DOMAIN 705 751
 DOMAIN 287 345
 SITE 740 743
 ACT_SITE 301 302
 DISULFID 291 341
 DISULFID 300 324
 DISULFID 316 337
 CARBOHYD 523 523
 CARBOHYD 552 552
 SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;
 Query Match 100.0%; Score 217; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 42
 DB 653 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGGVIA 694
 RESULT 8
 A4_HUMAN STANDARD; PRT; 770 AA.
 ID: A4_HUMAN
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP OR A4 OR CVAP OR ADL.
 DE Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RX Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RA "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
 RT Nature 325:733-736(1987).
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
 RA "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors.";
 RT Nature 331:525-527(1988).
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,

RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RA MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RA MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RA MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RA MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RA MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RA MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RA TISSUE=Liver;
 RC MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RA MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts";
 RL J. Biol. Chem. 262:8508-8514(1987).

RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,
 RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-mimetic
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;

RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide A beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykx T., Weidemann A., Muthaupt G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 Qy 1 DAERHDSGYEVHOKLVFFAEVDGSKNGAIGLMVGWVIA 42
 Db 672 DAERHDSGYEVHOKLVFFAEVDGSKNGAIGLMVGWVIA 713

Query Match 100.0%; Score 217; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN=BAUB/c; TISSUE=Brain;
 RA MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]

RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RX TISSUE=Brain, and Kidney; PubMed=2493250;
 RC MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(595),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X59379; -; NOT_ANNOTATED_CDS.
 CC EMBL; M18373; AAA37139.1; -;
 CC EMBL; X15210; CAA33280.1; -;
 CC EMBL; D10603; BAA01456.1; -;
 CC EMBL; M24397; AAA39929.1; -;
 CC PIR; A27485; A27485.
 CC PIR; S04855; S04855.
 CC PIR; S19727; S19727.
 CC HSSP; P05067; LAAP.
 CC MGD; MGI:88059; App.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR001255; Beta_APP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF03494; Beta_APP; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC PRINTS; PR00759; BASICPTASE.
 CC ProDom; PD000222; Kunitz_BPTI; 1.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT DOMAIN 18 699
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723
 FT POTENTIAL.
 FT DOMAIN 724 770
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715
 FT EQUIVALENT OF BETA-AMYLOID PROTEIN.

```

FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
FT VARSPLIC 346 380 MISSING (IN ISOFORM APP(751)).
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

Query Match 91.2%; Score 198; DB 1; Length 770;
Best Local Similarity 92.9%; Pred. No. 3.4e-18;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGVVIA 42
Db 672 DAEFGHDSGFEVRHQKLVFAEDVGSNKGAIIGLMVGVVIA 713

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL; X07648; CAA30488.1; -
CC EMBL; X14066; CAA32229.1; -

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DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSP: P05067; IAA.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_Bpti.
DR Pfam; PF00014; Kunitz_Bpti; 1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODom; PD000222; Kunitz_Bpti; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770 BY SIMILARITY.
FT DOMAIN 18 699 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 724 770 POTENTIAL.
FT DOMAIN 673 715 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT SITE 759 762 BPTI/KUNITZ INHIBITOR.
FT DISULFID 291 341 CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 91.2%; Score 198; DB 1; Length 770;
Best Local Similarity 92.9%; Pred. No. 3.4e-18;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGVVIA 42
Db 672 DAEFGHDSGFEVRHQKLVFAEDVGSNKGAIIGLMVGVVIA 713

RESULT 11
TR2M_AGR74
ID TR2M_AGR74 STANDARD; PRT; 755 AA.
AC P04029;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN TWS1.
OS Agrobacterium tumefaciens (strain Ach5), and
OS Agrobacterium tumefaciens.
OG Plasmid pTiAch5, and plasmid pTiA6NC.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176298, 358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ach5; PLASMID=pTiAch5;
RX MEDLINE=84207942; PubMed=6327292;
RA Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
RA Lemmers M., van Montagu M., Schell J.;
RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium
RT tumefaciens plasmid pTiAch5.";
RL EMBO J. 3:835-846(1984).
RN [2]
RP SEQUENCE FROM N.A.

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DR EMBL; X54058; CAA37993.1; -;
 DR PIR; S11549; S11549.
 DR InterPro; IPR001592; Poty_coat.
 DR Pfam; PF00767; Poty_coat; 1.
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
 FT NON_TER 1
 FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 61 327 COAT PROTEIN.
 SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DE6F2F18 CRC64;

Query Match 26.38; Score 57; DB 1; Length 327;
 Best Local Similarity 53.18; Pred. No. 3.7;
 Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHHQKLVFFAED----VGSNK 28
 DB 47 DDEFFDS-YEVHHQ-----ANDTIDAVGDNK 72

RESULT 14
 Y226_MYCPN STANDARD; PRT; 503 AA.
 AC P75462;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG226 homolog (F10_orf503).
 GN MPN319 OR MP517.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: TO M.GENITALIUM MG225.

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DR EMBL; AE000051; AAB96165.1; -;
 DR InterPro; IPR002293; AA/rel.prmease1.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa-permeases; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 20 40 POTENTIAL.
 FT TRANSMEM 43 63 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 215 235 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT TRANSMEM 301 321 POTENTIAL.
 FT TRANSMEM 359 379 POTENTIAL.
 FT TRANSMEM 405 425 POTENTIAL.
 FT TRANSMEM 443 463 POTENTIAL.
 FT TRANSMEM 468 488 POTENTIAL.
 SQ SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match 26.38; Score 57; DB 1; Length 503;
 Best Local Similarity 61.18; Pred. No. 5.7;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 24 VGSNKGAIIGLMVGGVV 41
 DB 131 VKDNGALLIGLVGGFVL 148

RESULT 15
 SLG1_YEAST STANDARD; PRT; 378 AA.
 ID SLG1_YEAST
 AC P54867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SLG1 protein precursor.
 GN SLG1 OR YOR008C OR UNF378.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA de Bettignies G., Bergez-Aullo P., Barthe C., Louvet O.,
 RA Peyrouquet M.F., Morel C., Doignon F., Crouzet M.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97051599; PubMed=8896276;
 RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
 RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
 RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
 RT which correspond to previously identified genes.";
 RL Yeast 12:1091-1095(1996).

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DR EMBL; U39481; AAA85862.1; -;
 DR EMBL; U43491; AAC49488.1; -;
 DR EMBL; Z74916; CAA99196.1; -;
 DR SGD; S0005534; SLG1.
 DR InterPro; IPR002889; WSC.
 DR Pfam; PF01822; WSC; 1.
 DR SMART; SM00321; WSC; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 378 SLG1 PROTEIN.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 378 AA; 39270 MW; EEEL64F2374CCCE3 CRC64;

Query Match 26.08; Score 56.5; DB 1; Length 378;
 Best Local Similarity 42.48; Pred. No. 5;
 Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

QY 8 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
 DB 251 SGSKTHKK-----ANVGAIVGGVGGVV 274

Search completed: April 21, 2003, 12:06:47
 Job time : 14 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:05:20 ; Search time 18 seconds
(without alignments)
224.314 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 247

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSNKGAIIGLMVGGVVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	217	100.0	42	2	PN0512
2	217	100.0	57	2	E60045
3	217	100.0	57	2	F60045
4	217	100.0	57	2	G60045
5	217	100.0	57	2	D60045
6	217	100.0	57	2	B60045
7	217	100.0	82	2	PQ0438
8	217	100.0	57	2	B60045
9	217	100.0	695	1	A49795
10	217	100.0	770	1	QRHUA4
11	198	91.2	695	2	A27485
12	198	91.2	695	2	S00550
13	198	91.2	747	2	JH0773
14	133	61.3	33	2	S23094
15	63	29.0	755	2	AI3228
16	62	28.6	755	1	QOAGAT
17	61	28.1	755	1	DAAGWT
18	57	26.3	37	2	S11435
19	57	26.3	503	2	S73843
20	56.5	26.0	378	2	S61992
21	55.5	25.6	297	2	G69525
22	55.5	25.6	678	2	G71526
23	55	25.3	291	2	F95015
24	55	25.3	317	2	H97888
25	55	25.3	488	2	S27652
26	55	25.3	3063	2	JS0166
27	54.5	25.1	678	2	C81683
28	54.5	25.1	832	2	H84848
29	54	24.9	77	2	C97027

30 54 24.9 284 2 S04723
31 54 24.9 763 2 AI3443
32 53.5 24.7 708 2 T24727
33 53.5 24.7 971 2 D70128
34 53 24.4 256 2 G6774
35 35 24.4 390 2 C75103
36 53 24.4 422 2 D72302
37 53 24.4 601 2 T02581
38 53 24.4 1555 2 JT0959
39 52.5 24.2 314 2 F86805
40 52.5 24.2 678 2 C86495
41 52.5 24.2 678 2 H72128
42 52 24.0 272 2 F70979
43 52 24.0 339 2 A81351
44 52 24.0 417 2 F70132
45 52 24.0 527 2 T18232

ALIGNMENTS

RESULT 1

PN0512

beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653; PMID:7685598

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SHI>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 217; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 7.5e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEVDVGSNKGAIIGLMVGGVVIA 42

||||| 1 DAEFRHDSGYEVHHQKLVFFAEVDVGSNKGAIIGLMVGGVVIA 42

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in r

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEVDVGSNKGAIIGLMVGGVVIA 42

||||| 6 DAEFRHDSGYEVHHQKLVFFAEVDVGSNKGAIIGLMVGGVVIA 47

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CAA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 47

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; G60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MUID:93075180; PMID:1445331

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 217; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.6e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 42

|||||

Db 17 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 58

RESULT 9

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A49795

R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p

A:Reference number: A49795; MUID:91273117; PMID:1905108

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C:Keywords: alternative splicing

Query Match 100.0%; Score 217; DB 1; Length 695;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 42

|||||

Db 597 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIA 638

RESULT 10

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44

4668; A28583; A29302; A60805; JF0038; S06121; A60355; A59011; A38384; S29076; S38252; S3

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b

A:Reference number: S02260; MUID:89128427; PMID:2783775

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288,'V',365-770 <LEM1>

A:Cross-references: EMBL:X13466

A>Note: alternative splice form APP(695)

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:g355598; PIDN:CAA31830.1; PID:g871360

A>Note: alternative splice form APP(695)

R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870; PMID:2538123

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030; PMID:2675837

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865

R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, P

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid

A:Reference number: A35486; MUID:90321244; PMID:2196878

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PREI>

A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients

R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 87, 257-263, 1990

A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318; PMID:2110105

A:Accession: I39452

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Residues: 1-770 <YOS1>

A:Molecule type: DNA

A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616

A:Accession: I39451

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-530,'QWLMPVIPAFAWEAKYGR' <YOS2>

A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615

R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 102, 291-292, 1991

A:Reference number: A59020; MUID:91340168; PMID:1908403

A:Contents: annotation; erratum

A>Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du

Science 248, 1124-1126, 1990

A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hem

A:Reference number: I39453; MUID:90260663; PMID:2111584

A:Accession: I39453

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <LEV>

A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620

A>Note: a mutation with 693-Gln is presented

R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.

Science 254, 97-99, 1991

A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe

A:Reference number: I59562; MUID:92022553; PMID:1925564

A:Accession: I59562

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-716,'F',718-737 <MUR>

A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721

R:Kanino, K.; Orr, H.T.; Payami, H.; Wajzman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders

arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart

Am. J. Hum. Genet. 51, 998-1014, 1992

A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for r

A:Reference number: A44017; MUID:93035397; PMID:1415269

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692,'G',694-718 <KAM1>

A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378

A:Experimental source: familial Alzheimer disease family SB

A>Note: sequence extracted from NCBI backbone (NCBIP:115374)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AA23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface protein
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:X00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular amyloid precursor protein
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C. Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid precursor protein
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, J.L.; Gusella, J.F.; Nature 325, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer's disease locus
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muellemeier, J.; Nature 331, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor protein
A:Reference number: S02638; MUID:88226437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.; Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De Strooper, B.; Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor activity
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>

A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three Alzheimer's disease patients
A:Reference number: A03020
A:Accession: A03020
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B03020
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C03020
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 611 as Gly
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottinger, J.; Martins, R.N.; Beyreuther, K. Nature 325, 528-530, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer's disease locus
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muellemeier, J.; Nature 331, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor protein
A:Reference number: S02638; MUID:88226437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.; Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De Strooper, B.; Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor activity
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>

Matches 16; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

Qy 7 DSGYEVHHQKLVFFAEDYGSNKGAIIGLWVGCVIA 42
 Db 223 DSG-----RIGFFPEDYVKKVAIIGAGISGLVVA 252

Search completed: April 21, 2003, 12:07:46
 Job time : 20 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 11:57:04 ; Search time 36 Seconds
(without alignments)
155.459 Million cell updates/sec

Title: US-09-580-018-42
Perfect score: 217
Sequence: 1 DAEPFRHDSGVVHHQKLVFF.....DVGSNGAIIGLMVGWVIA 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	42	13 AAR20330	Sequence of A99 (b
2	217	100.0	42	15 AAR60366	Beta-amyloid (1-42
3	217	100.0	42	17 AAR95248	Beta/A4-amyloid pe
4	217	100.0	42	17 AAR94591	Alzheimer amyloid
5	217	100.0	42	18 AAW12828	Beta A4 peptide.
6	217	100.0	42	19 AAW64507	Neurotoxic beta-am
7	217	100.0	42	19 AAW47230	Beta-amyloid pepti
8	217	100.0	42	19 AAW42989	Full length beta-a
9	217	100.0	42	20 AAY49691	Human beta amyloid
10	217	100.0	42	20 AAY33407	Human amyloidogeni

11	217	100.0	42	20 AAY25137	Human amyloid beta
12	217	100.0	42	20 AAV08607	Human beta-amyloid
13	217	100.0	42	20 AAW29093	A-beta-binding pep
14	217	100.0	42	20 AAW99585	Mutant aggregating
15	217	100.0	42	20 AAW92726	Human tachykinin a
16	217	100.0	42	20 AAW81474	Synthetic amyloid
17	217	100.0	42	21 AAY96956	Beta-amyloid 1-42
18	217	100.0	42	22 AAB82622	Amyloid-beta pepti
19	217	100.0	42	22 AAE05484	Human peptide anti
20	217	100.0	42	22 AAB86134	Human Alzheimer-be
21	217	100.0	42	22 AAB91779	Amyloid beta-prote
22	217	100.0	42	22 AAB91812	Amyloid beta-prote
23	217	100.0	42	22 AAB49098	Human amyloid beta
24	217	100.0	42	22 AAB48497	Human amyloid prot
25	217	100.0	42	22 AAB48830	Human amyloid-beta
26	217	100.0	42	22 AAB49395	Human amyloid pept
27	217	100.0	42	22 AAB35589	Beta/A4-amyloid pe
28	217	100.0	42	23 AAB98727	Human amyloid beta
29	217	100.0	42	23 ABB83306	Amyloid-beta (Abet
30	217	100.0	42	23 AUB96896	Human Amyloid beta
31	217	100.0	42	23 ABB81321	Amyloid precursor
32	217	100.0	42	23 AAE21438	Human beta-amyloid
33	217	100.0	42	23 ABB76029	Beta amyloid pepti
34	217	100.0	42	23 AAU93988	Human beta-amyloid
35	217	100.0	42	23 AAU76483	Amino acids 1-42 o
36	217	100.0	42	23 AAU80961	Human amyloid beta
37	217	100.0	42	23 AAG68314	Human beta amyloid
38	217	100.0	42	23 AAM51864	Neuronal death inh
39	217	100.0	42	23 AAU75433	Amyloid peptide pr
40	217	100.0	43	10 AAP96371	Region of pre-AβC
41	217	100.0	43	15 AAR54759	Beta amyloid pepti
42	217	100.0	43	15 AAR60367	Beta-amyloid (1-43
43	217	100.0	43	15 AAR61328	Amyloid beta-prote
44	217	100.0	43	16 AAR64165	Beta amyloid prote
45	217	100.0	43	17 AAR95673	A-beta protein (43

ALIGNMENTS

RESULT 1
AAR20330
ID AAR20330 standard; peptide; 42 AA.
XX
AC AAR20330;
XX
DT 14-APR-1992 (first entry)
XX
DE Sequence of A99 (beta-amyloid core domain).
XX
KW Transgenic mice; Alzheimer's disease; diagnosis;
beta-amyloid precursor; plaque core protein.
XX
OS Homo sapiens.
XX
PN WO9119810-A.
XX
PD 26-DEC-1991.
XX
PF 17-JUN-1991; 91WO-US04447.
XX
PR 15-JUN-1990; 90US-0538857.
XX
PA (CALB-) CALIF BIOTECHN INC.
XX
PI Cordell B;
XX
DR WPI; 1992-024426/03.
XX
PT Transgenic mice as models for studying Alzheimer's disease
proteins - contg. cells with promoter and beta-amyloid precursor
protein deoxyribonucleic acid, useful for testing
anti-alzheimer's drugs

```

XX PS Disclosure; Fig 3; 98pp; English.
XX CC The inventors specifically claim transgenic mice contg. DNA encoding
XX CC A42 (beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid
XX CC carboxy tail) (AAR20329), A695 (beta-amyloid precursor protein), A751
XX CC (precursor plus inhibitor) or A41 (protease inhibitor) (AAR20328).
XX CC Human fibroblast cDNA clone lambdaAPCP16814 was deposited at ATCC on
XX CC July 1, 1987 and has accession No. 40347. The promoter is pref. the
XX CC NSE promoter with the A751 or the A695 sequence.
XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 13; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 2
AAR60366
ID AAR60366 standard; peptide; 42 AA.
AC AAR60366;
XX 15-MAR-1995 (first entry)
XX Beta-amyloid (1-42).
DE Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.
KW Homo sapiens.
XX WO9417197-A.
XX 04-AUG-1994.
XX 24-JAN-1994; 94WO-JP00089.
XX 25-JAN-1993; 93JP-0010132.
XX 05-FEB-1993; 93JP-0019035.
XX 16-NOV-1993; 93JP-0286985.
XX 28-DEC-1993; 93JP-0334773.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Kitada C, Odaka A, Suzuki N;
XX WPI; 1994-264110/32.
XX Antibodies recognising specific parts of beta-amyloid - can be
XX used for diagnosis of diseases implicating beta-amyloid, such as
XX Alzheimer's disease
XX Disclosure; Page 83; 116pp; Japanese.
XX Antibodies which recognise specific subfragments of the beta-amyloid
XX protein are claimed. Specifically, the antibodies (which are pref.
XX monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
XX portion of beta-amyloid or they recognise residues 25-35 or 35-43
XX from the C-terminal portion. The antibodies are useful for assaying
XX beta-amyloid and its derivatives for diagnosis of Alzheimer's
XX disease.
XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 3
AAR95248
ID AAR95248 standard; peptide; 42 AA.
XX AAR95248;
XX 20-JAN-1997 (first entry)
XX Beta/A4-amyloid peptide.
XX Beta/A4-amyloid peptide; tissue plasminogen activator;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
KW haemorrhage.
XX Homo sapiens.
XX WO9615799-A1.
XX 30-MAY-1996.
XX 22-NOV-1995; 95WO-US15007.
XX 22-NOV-1994; 94US-0347144.
XX (RUFF ) UNIV RUTGERS STATE NEW JERSEY.
XX Anderson S;
XX WPI; 1996-268332/27.
XX Use of agents which bind beta-amyloid peptide - for diagnosis,
XX prevention and treatment of vascular damage caused by amyloid
XX deposits, partic. in haemorrhaging and Alzheimer's disease
XX Example 1; Fig 1; 52pp; English.
XX To investigate the effects of beta-amyloid peptide (BAP) on
XX tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
XX One peptide contained 42 amino acids and corresp. to the full
XX length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
XX the 28 N-terminal residues of the BAP found in Alzheimer's disease
XX and hereditary cerebral haemorrhage with amyloidosis-Dutch type
XX (HCHWA-D), respectively. In an assay to determine the effect of
XX the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
XX gave 1st order rate constant of activation (k(app)) values of
XX 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for nil
XX and fibrinogen controls. The results demonstrate that the BAP are
XX able to stimulate t-PA activity in vitro, which is significant in
XX that it provides a means for investigating and controlling the
XX pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
XX angiopathy related cerebral haemorrhage.
XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
AAR94591

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ID AAR94591 standard; peptide; 42 AA.
 AC AAR94591;
 XX
 DT 21-AUG-1996 (first entry)
 XX
 DE Alzheimer amyloid beta-protein active site sequence.
 XX
 KW Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;
 KW serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;
 KW complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.
 XX
 OS Synthetic.
 XX
 PN US5506097-A.
 XX
 PD 09-APR-1996.
 XX
 PF 24-AUG-1990; 90US-0572671.
 XX
 PR 10-JAN-1994; 94US-0179574.
 PR 24-AUG-1990; 90US-0572671.
 PR 13-JAN-1992; 92US-0819361.
 PR 13-JAN-1993; 93WO-US00325.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Kayyali U, Potter H;
 XX
 DR WPI; 1996-200270/20.
 XX
 PT Inhibiting enzymatic activity of Alzheimer amyloid beta-protein -
 PT using p-amidino:phenylmethanesulphonyl fluoride or ebelactone A,
 PT for treatment, study and diagnosis of Alzheimer's disease, etc.
 XX
 PS Disclosure; Fig 1; 17pp; English.
 XX
 CC This is the sequence of a fragment of the beta-amyloid protein
 CC associated with Alzheimer's disease. The protein contains esterase
 CC (cholinesterase and lipase) activities based on active site similarities
 CC with serine proteases (see AAR94592-96). The esterase activity of the
 CC beta-amyloid protein is inhibited by the cpds. of the invention i.e.
 CC ebelactone A or para-amidinophenylmethanesulphonyl fluoride. Inhibition
 CC of these activities prevent complex formation between the beta-amyloid
 CC protein and alpha(1)-antichymotrypsin, thus can be used to treat, study
 CC or diagnose Alzheimer's or Down's diseases or normal ageing.
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 217; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 RESULT 5
 AAW12828
 ID AAW12828 standard; peptide; 42 AA.
 AC AAW12828;
 XX
 DT 08-DEC-1997 (first entry)
 XX
 DE Beta A4 peptide.
 XX
 KW Beta A4 peptide; alzheimer's disease; peptide aggregation; brain;
 KW therapy; inhibitor.
 XX
 OS Homo sapiens.
 XX

PN WO9707403-A1.
 XX
 PD 27-FEB-1997.
 XX
 PF 23-JUL-1996; 96WO-US12034.
 XX
 PR 16-AUG-1995; 95US-0515606.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 XX
 DR WPI; 1997-165447/15.
 XX
 PT Determn. of the degree of betaA4 peptide aggregation using binding
 PT agent - used to screen cpds. for possible use in Alzheimer's disease
 PT treatment
 XX
 PS Disclosure; Page 10; 18pp; English.
 XX
 CC This sequence represents the beta A4 peptide. The degree of aggregation
 CC of this peptide is determined using the method of the invention. The beta
 CC A4 peptide is present in the brain of Alzheimer's disease patients, but
 CC not in the brain of non-Alzheimer's disease individuals. The peptide
 CC clumps or aggregates in the brain of Alzheimer's disease patients, where
 CC it may be responsible for the destruction of normal brain cells. Once the
 CC clumps or aggregates form, the formulation is almost irreversible. The
 CC method of the invention comprises reacting this sequence with a binding
 CC reagent capable of binding to it only in its non-aggregated state, to
 CC form an amount of a beta A4 peptide-bound reagent and an amount of
 CC protein free reagent. The amount of the beta A4 peptide, binding reagent
 CC complex is then measured. Compounds which inhibit aggregation of beta A4
 CC peptide are potentially useful for treatment of Alzheimer's disease.
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 217; DB 18; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 RESULT 6
 AAW64507
 ID AAW64507 standard; peptide; 42 AA.
 AC AAW64507;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Neurotoxic beta-amyloid peptide decoy peptide #20.
 XX
 KW Beta-amyloid peptide; beta-AP; neurotoxin; calcium influx;
 KW aggregate; Alzheimers disease; decoy; treatment.
 XX
 OS Synthetic.
 XX
 PN WO9830229-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 09-JAN-1998; 98WO-US000653.
 XX
 PR 29-OCT-1997; 97US-0960188.
 PR 10-JAN-1997; 97US-0035847.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Blanchard BJ, Ingram VM;
 XX

DR WPI; 1998-398795/34.
 XX Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor,
 PT useful for, e.g. treating Alzheimer's disease
 XX
 PS Example 8; Page 46; 68pp; English.
 XX
 CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
 CC form aggregates that increase calcium influx into neuronal cells. Such
 CC peptides can be used in the treatment of diseases associated with
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
 CC injection and orally, or from slow-release implants.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 7
 AAW47230
 ID AAW47230 standard; peptide; 42 AA.
 AC- AAW47230;
 XX
 XX 22-MAY-1998 (first entry)
 DT
 DE Beta-amyloid peptide residues 1-42.
 XX
 XX Screening assay; beta-amyloid peptide; treatment;
 KW amyloidosis disease; Alzheimer's disease.
 KW Homo sapiens.
 OS
 XX US5721106-A.
 PN
 XX 24-FEB-1998.
 PD
 XX 12-SEP-1994; 94US-0304585.
 PF
 XX 12-SEP-1994; 94US-0304585.
 PR 13-AUG-1991; 91US-0744767.
 XX
 XX (HARD) HARVARD COLLEGE.
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Magglo JE, Mantyh PW;
 DR WPI; 1998-168404/15.
 XX
 PT New in vitro screening assay for Alzheimer's disease drugs -
 PT comprises assessing binding of labelled beta-amyloid peptide to silk
 PT sample
 XX
 PS Claim 8; Columns 29-30; 36pp; English.
 XX
 CC The present sequence was used in the development of a novel in
 CC vitro screening assay for agents capable of affecting the
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method
 CC comprises contacting a silk sample with labelled BAP, optionally
 CC in the presence of a test agent, detecting the amount of label
 CC bound to the silk and assessing the effect of the agent on the
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are
 CC potentially useful for treating amyloidosis diseases, especially
 CC Alzheimer's disease.

XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 8
 AAW42989
 ID AAW42989 standard; peptide; 42 AA.
 XX
 AC AAW42989;
 XX
 XX 01-MAY-1998 (first entry)
 DT
 DE Full length beta-amyloid peptide (BAP).
 XX
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage.
 XX
 OS Homo sapiens.
 XX
 XX US5703209-A.
 PN
 XX 30-DEC-1997.
 PD
 XX 05-JUN-1995; 95US-0464248.
 PF
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 PI Jacobsen JS, Vitek MP;
 XX
 XX WPI; 1998-076482/07.
 DR
 PT Amyloid precursor protein fusion polypeptides - comprising APP
 PT fragment and marker, useful for research and drug screening
 XX
 PS Disclosure; Column 7; 84pp; English.
 XX
 CC The present sequence represents a beta-amyloid peptide (BAP). Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16Lys and 17Leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
 CC APP-770. These isoforms are derived by alternative splicing. APP-APP 751
 CC is a deletion construct of APP-751, which has a deletion of 276 amino
 CC acids to within 15 amino acids of the BAP domain. APP can be used as a
 CC substrate for studying abnormal proteolytic cleavage which results in the
 CC release of BAP, and also to screen for drugs that will inhibit such
 CC cleavage.
 XX
 XX Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 9

AA49691

ID AAY49691 standard; peptide; 42 AA.

XX AC AAY49691;

XX DT 13-JAN-2000 (first entry)

XX DE Human beta amyloid precursor protein peptide.

XX KW Human; beta amyloid precursor protein; APP; beta secretase inhibition;
KW alpha secretase; neurological disorder; Alzheimer's disease;
KW Downs syndrome; mutation.

XX OS Homo sapiens.

XX PN WO9951752-Al.

XX PD 14-OCT-1999.

XX PF 31-MAR-1999; 99WO-JP01701.

XX PR 31-MAR-1998; 98JP-0101821.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Ozawa K, Ikeda S, Tabira T;

XX DR WPI; 1999-620208/53.

XX PT A cell line which produces beta amyloid precursor protein, used in the
PT investigation of neurological disorders such as Alzheimer's disease -

XX PS Disclosure; Page 41; 70pp; Japanese.

XX CC The present invention describes a cell line which produces beta amyloid
CC precursor protein (APP) and expresses alpha secretase activity but
CC expresses beta secretase activity only under an external stimulus.
CC Also described is a cloning method for DNA encoding beta secretase,
CC comprising: (1) inserting a DNA library into the cell line, expressing
CC the inserted DNA, and selecting cells expressing beta secretase,
CC isolating the beta secretase DNA from them; or (2) isolating nucleic
CC acid from the cell line with or without external stimulation and
CC performing subtractive cloning to identify DNA expressed only under
CC stimulation. Products from the present invention may be used in the
CC investigation of neurological disorders such as Alzheimer's disease
CC and Downs syndrome and in particular the association of mutations of
CC the beta APP with them. The present sequence represents a human
CC beta APP peptide.

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.2e-25;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 10

AA49691

ID AAY33407 standard; peptide; 42 AA.

XX AC AAY33407;

XX DT 03-DEC-1999 (first entry)

XX DE Human amyloidogenic A-beta peptide 1.

XX

KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW Down's Syndrome.

XX OS Homo sapiens.

XX PN WO9941279-A2.

XX PD 19-AUG-1999.

XX PF 12-FEB-1999; 99WO-US03231.

XX PR 13-FEB-1998; 98US-0074658.

XX PA (ARCH-) ARCH DEV CORP.

XX PI Lynn DG, Meredith SC, Burkoth TS;

XX PN WPI; 1999-561326/47.

XX PT Inhibiting amyloid plaque formation in humans suffering from
PT amyloidosis, Alzheimer's disease or Down's Syndrome -

XX PS Claim 21; Page 140; 141pp; English.

XX CC This invention describes a novel method for inhibiting amyloid
CC fibrillogenesis which comprises contacting tissue with a composition
CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC at an end terminal or a side chain, by conjugation to polyethylene
CC glycol, by conjugation to a second compound and a pharmaceutically
CC acceptable buffer, solvent or diluent. The methods are used to inhibit
CC amyloid plaque formation in humans suffering from amyloidosis,
CC Alzheimer's disease or Down's Syndrome. This sequence represents a
CC fragment of the beta-amyloid peptide described in the method of the
CC invention.

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.2e-25;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 11

AA49691

ID AAY25137 standard; peptide; 42 AA.

XX AC AAY25137;

XX DT 26-AUG-1999 (first entry)

XX DE Human amyloid beta-A4 peptide 5.

XX KW Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
KW therapeutic drug; brain; Alzheimer's disease.

XX OS Homo sapiens.

XX PN US5919631-A.

XX PD 06-JUL-1999.

XX PF 17-JUL-1996; 96US-0682245.

XX PR 17-JUL-1996; 96US-0682245.

XX PA (HMRI) HOECHST MARION ROUSSEL INC.

PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 XX WPI; 1999-403957/34.
 XX Determination of degree of aggregation of a peptide, useful for
 PT identifying therapeutic drugs for treating Alzheimer's disease
 XX
 XX Claim 1; Column 7-8; 8pp; English.
 XX
 CC This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated
 CC (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to
 CC unaggregated (I); (b) measuring the amount of (II) bound to (I) to
 CC obtain a value (i); (c) repeating steps (a) and (b) with a second
 CC sample at a different time to obtain a second value (ii); and (d)
 CC determining the difference between (i) and (ii) which is inversely
 CC related to the degree of aggregation of (I). This method may be
 CC applied to a screen for compounds that inhibit aggregation of (I).
 CC These inhibitors may be used as therapeutic drugs to inhibit the
 CC formation of these aggregates in the brains of patients suffering
 CC from Alzheimer's disease.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 12
 AAY08607
 ID AAY08607 standard; Protein; 42 AA.
 XX
 AC AAY08607;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 XX Human beta-amyloid precursor core protein A42.
 DE
 XX APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
 KW Alzheimer's disease; model; therapeutic compound; brain; mechanism;
 KW nerve tissue specific promoter; synthesis; inhibitor; deposition;
 KW plaque formation; treatment; A42.
 XX
 OS Homo sapiens.
 XX
 PN US5912410-A.
 XX
 PD 15-JUN-1999.
 XX
 PF 13-APR-1995; 95US-0422333.
 XX
 PR 21-OCT-1994; 94US-0327381.
 PR 15-JUN-1990; 90US-0538857.
 PR 17-JUN-1991; 91US-0716725.
 PR 13-APR-1995; 95US-0422333.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI Cordell B;
 XX
 XX WPI; 1999-357231/30.
 XX
 XX Transgenic mice useful for studying compounds potentially useful in
 PT the treatment of Alzheimer's disease
 XX
 XX Disclosure; Fig 3; 72pp; English.
 PS
 XX

CC This invention describes novel transgenic mice expressing proteins
 CC related to the pathology of Alzheimer's disease and which provide models
 CC for studying potentially therapeutic compounds. The transgenic mice
 CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)
 CC and a nerve tissue specific promoter operably linked to the beta-APP
 CC allowing its expression to form beta-amyloid protein deposits in the
 CC animal's brain. The transgenic mouse is useful for elucidating the
 CC molecular mechanisms involved in the synthesis of and, more importantly,
 CC inhibiting the synthesis and deposition of beta-amyloid proteins (most
 CC importantly in the brain where plaque formation is associated with
 CC Alzheimer's disease) by inhibiting production and/or increasing cleavage
 CC after production. The transgenic animals provide useful models for
 CC studying the in vivo relationships of the proteins to each other and to
 CC other compounds being tested for their usefulness in treating Alzheimer's
 CC disease.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
 RESULT 13
 AAW29093
 ID AAW29093 standard; peptide; 42 AA.
 XX
 AC AAW29093;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 XX A-beta-binding peptide 1-42.
 DE
 XX Cyclosporin; A-beta peptide; conjugate; neurological disease;
 KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
 KW ALS; non-immunosuppressive; amyloid plaque formation.
 XX
 OS Homo sapiens.
 XX
 PN WO9910374-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 25-AUG-1998; 98WO-US17544.
 XX
 PR 26-AUG-1997; 97US-0057751.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Rich DH, Solomon ME;
 XX
 XX WPI; 1999-276928/23.
 DR
 XX New A-beta-binding peptide conjugates and CSA analogs - useful in
 PT treatment of neurological diseases e.g. Alzheimer's disease,
 PT multiple sclerosis etc.
 XX
 XX Claim 5; Page 98; 129pp; English.
 XX
 XX New conjugates are disclosed which are of formula A-Z, in which: A is
 CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
 CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
 CC contiguous residues of A-beta peptide. The compounds are novel chemical
 CC inducers of dimerization which are non-immunosuppressive and which are
 CC inhibitors of A-beta peptide aggregation and deposition in amyloid
 CC plaques. The adverse consequences of amyloid plaque formation can be
 CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
 CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
 CC therefore providing a mechanism to minimize the amount of free A-beta

CC available for fibril formation and deposition. The compounds can be used
CC for the treatment of Alzheimer's disease, multiple sclerosis and
CC amyotrophic lateral sclerosis.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 14

AAW9585
ID AAW9585 standard; peptide; 42 AA.

XX AC AAW9585;

XX DT 22-JUN-1999 (first entry)

XX DE Mutant aggregating amyloid-beta peptide.

XX KW Aggregation; amyloid-beta peptide; fluorescent group; detection;
XX diagnosis; Alzheimer's disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN W09908695-A1.

XX PD 25-FEB-1999.

XX PF 13-AUG-1998; 98WO-US16809.

XX PR 14-AUG-1997; 97US-0055660.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Garzon-Rodriguez W, Glabe C;

XX DR WPI; 1999-190112/16.

XX PT New fluorescent labeled amyloid A-beta peptides

XX PS Example 1; Page 21; 50pp; English.

XX CC This sequence corresponds to a mutant aggregating amyloid-beta peptide
CC which can be covalently labelled with a fluorescent group. The detection
CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
CC or detect a predisposition to Alzheimer's disease. The screening assays
CC can be used to identify compounds for the treatment or amelioration of
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
CC amyloid-beta peptide are also useful for exploring other aspects of
CC amyloid structure.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
|||||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 15

AAW92726

ID AAW92726 standard; peptide; 42 AA.

XX

AC AAW92726;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #72.

XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX PN US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 41-42; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
CC with amyloidosis, and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92555-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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